

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:13:17 ; Search time 122 Seconds  
(without alignments)  
208.189 Million cell updates/sec

Title: US-09-809-060A-2  
Perfect score: 36  
Sequence: 1 YNTNTYTLLESQNOQKNEQELLELDKWSLWNWF 36

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 2166443 seqs, 705528306 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Uniprot 05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

⚡ Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	122	2	Q6WH50_9HIV1
2	36	100.0	853	2	Q80161_9HIV1
3	36	100.0	855	1	ENV_HV1A2
4	32	88.9	122	2	Q7ZJR9_9HIV1
5	32	88.9	122	2	Q9EA82_9HIV1
6	32	88.9	122	2	Q9LJN5_9HIV1
7	32	88.9	127	2	Q6V822_9HIV1
8	32	88.9	141	2	Q6V8Y8_9HIV1
9	32	88.9	144	2	Q7ZC84_9HIV1
10	32	88.9	144	2	Q7ZCE4_9HIV1
11	32	88.9	845	2	Q6VA57_9HIV1
12	32	88.9	852	1	ENV_HV1S3
13	32	88.9	852	2	Q92761_9HIV1
14	32	88.9	852	2	Q73303_9HIV1
15	32	88.9	855	2	Q9E1R7_9HIV1
16	32	88.9	858	2	Q8Q865_9HIV1
17	32	88.9	858	2	Q8Q867_9HIV1
18	32	88.9	859	2	Q8Q863_9HIV1
19	32	88.9	860	2	Q9E1S7_9HIV1
20	32	88.9	864	2	Q9E610_9PLVG
21	32	88.9	871	2	Q5D7P6_9HIV1
22	32	88.9	871	2	Q5D7Q3_9HIV1
23	29	80.6	122	2	Q9EAA5_9HIV1
24	29	80.6	122	2	Q9YXN9_9HIV1
25	29	80.6	122	2	Q9YXR6_9HIV1
26	29	80.6	138	2	Q5UC10_9HIV1
27	29	80.6	144	2	Q7ZC86_9HIV1
28	29	80.6	144	2	Q7ZC94_9HIV1
29	29	80.6	144	2	Q7ZCB0_9HIV1
30	29	80.6	144	2	Q7ZCB1_9HIV1
31	29	80.6	144	2	Q7ZCB7_9HIV1

32	29	80.6	144	2	Q7ZCE3_9HIV1	Q7zce3 human immun
33	29	80.6	199	2	Q8JAL6_9HIV1	Q8jal6 human immun
34	29	80.6	845	2	Q6JEL6_9HIV1	Q6jel6 human immun
35	29	80.6	849	2	Q6EFV9_9HIV1	Q6efv9 human immun
36	29	80.6	849	2	Q7ZC12_9HIV1	Q7zc12 human immun
37	29	80.6	849	2	Q7ZC14_9HIV1	Q7zc14 human immun
38	29	80.6	850	2	Q6B4P1_9HIV1	Q6b4p1 human immun
39	29	80.6	858	2	Q6BC08_9HIV1	Q6bc08 human immun
40	29	80.6	859	2	Q72940_9HIV1	Q72940 human immun
41	29	80.6	868	2	Q7ZC11_9HIV1	Q7zc11 human immun
42	29	80.6	868	2	Q7ZC13_9HIV1	Q7zc13 human immun
43	27	75.0	42	2	Q69910_9HIV1	Q69910 human immun
44	27	75.0	117	2	Q6WH02_9HIV1	Q6wh02 human immun
45	27	75.0	120	2	Q4VUP4_9HIV1	Q4vup4 human immun

## ALIGNMENTS

RESULT 1  
Q6WH50\_9HIV1 PRELIMINARY; PRT; 122 AA.  
AC Q6WH50;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=14715797; DOI=10.1128/JCM.42.1.426-430.2004;  
RA Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,  
RA Couvea M.I.F.S., Guimarães M.A.M., De Oliveira F.E.,  
RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;  
RT "Prevalence of human immunodeficiency virus drug resistance mutations and subtypes in drug-naïve, infected individuals in the army health service of Rio de Janeiro, Brazil";  
RT J. Clin. Microbiol. 42:426-430(2004).  
RL EMBL; AY285046; AAQ68109.1; -; Genomic\_RNA.  
DR SRR; Q6WH50; 1-105.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; P:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Fram; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14775 MW; 66674BB2877E73FB CRC64;  
Query Match 100.0%; Score 36; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 2.9e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 YNTNTYTLLESQNOQKNEQELLELDKWSLWNWF 36  
Db 78 YNTNTYTLLESQNOQKNEQELLELDKWSLWNWF 113  
RESULT 2  
Q80161\_9HIV1 PRELIMINARY; PRT; 853 AA.  
AC Q80161;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
DE Envelope polypeptide.  
GN Name=env;  
OS Human immunodeficiency virus 1.

OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
 OC Lentivirus; Primate lentivirus group.  
 RN [1] NCBI\_TaxID=11676;  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=92046357; PubMed=1658383;  
 RA Cheng-Mayer C., Shioda T., Levy J.A.;  
 RT "Host range, replicative, and cytopathic properties of human  
 RT immunodeficiency virus type 1 are determined by very few amino acid  
 RT changes in tat and gp120";  
 RL J. Virol. 65:6931-6941(1991).  
 DR ENBL; L07422; AAA80324.1; -; Genomic\_RNA.  
 DR HSP; P04578; 1DLB.  
 DR SMR; Q80161; 198-488, 529-623.  
 DR GO; GO:0016021; C: integral to membrane; IEA.  
 DR GO; GO:0019031; C: viral envelope; IEA.  
 DR GO; GO:0005198; F: structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Envelope protein; Polypeptide; Transmembrane.  
 SQ SEQUENCE 853 AA; 97056 MW; 2181503CFD14789 CRC64;  
 Query Match 100.0%; Score 36; DB 2; Length 853;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-26;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 36  
 DB 635 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 670  
 RESULT 3  
 ENV\_HVIA2  
 ID ENV\_HVIA2 STANDARD; PRT; 855 AA.  
 AC P03378;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane  
 DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
 GN Names=Env;  
 OS Human immunodeficiency virus type 1 (isolate ARV2/SP2) (HIV-1).  
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
 OC Lentivirus; Primate lentivirus group.  
 OC NCBI\_TaxID=11685;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [GENOMIC RNA].  
 RX MEDLINE=85090453; PubMed=2578227;  
 RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,  
 RA Stempien M.M., Brown-Shiner S.L., Gee W.W., Renard A., Randolph A.,  
 RA Levy J.A., Dina D., Luciw P.A.;  
 RT "Nucleotide sequence and expression of an AIDS-associated retrovirus  
 RT (ARV-2).";  
 RL Science 227:484-492(1985).  
 CC -----  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use as long as its content is in no way modified and this statement is not  
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 CC -----  
 DR ENBL; K02007; AAB59882.1; -; Genomic\_RNA.  
 DR PIR; A03976; VCLJ2A.  
 DR HSP; P04578; 1DLB.  
 DR SMR; P03378; 199-490, 539-625.  
 DR HIV; K02007; ENV5SF2.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR InterPro; IPR000777; GP120.  
 DR Pfam; PF00516; GP120; 1.  
 DR Pfam; PF00517; GP41; 1.  
 KW AIDS; Capsid protein; Glycoprotein; Polypeptide; Signal;

KW Structural protein; Transmembrane.  
 FT SIGNAL 1 29  
 FT CHAIN 30 509 Exterior membrane glycoprotein.  
 FT CHAIN 510 855 Transmembrane glycoprotein.  
 FT CARBOHYD 87 87 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 129 129 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 140 140 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 154 154 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 158 158 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 184 184 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 190 190 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 200 200 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 233 233 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 244 244 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 265 265 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 279 279 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 292 292 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 298 298 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 304 304 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 334 334 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 341 341 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 358 358 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 364 364 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 388 388 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 394 394 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 400 400 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 408 408 N-linked (GlcNAc...) (Potential).  
 FT CARBOHYD 445 445 N-linked (GlcNAc...) (Potential).  
 FT DISULFID 53 73 By similarity.  
 FT DISULFID 118 208 By similarity.  
 FT DISULFID 125 199 By similarity.  
 FT DISULFID 130 155 By similarity.  
 FT DISULFID 221 250 By similarity.  
 FT DISULFID 231 242 By similarity.  
 FT DISULFID 299 333 By similarity.  
 FT DISULFID 380 442 By similarity.  
 FT DISULFID 387 435 By similarity.  
 SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;  
 Query Match 100.0%; Score 36; DB 1; Length 855;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-26;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 36  
 DB 637 YNTTYTLLSESONQOEKNEQELLELDKWSLWNWF 672  
 RESULT 4  
 Q7ZJR9\_9HIV1  
 ID Q7ZJR9\_9HIV1 PRELIMINARY; PRT; 122 AA.  
 AC Q7ZJR9;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Envelope glycoprotein (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
 OC Lentivirus; Primate lentivirus group.  
 OC NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=22800244; PubMed=12921095; DOI=10.1089/088922203223221003;  
 RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;  
 RT "Molecular Characterization of 39 HIV-1 Isolates Representing Group M

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RT (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol
RT integrase, and env gp41.
RL AIDS Res. Hum. Retroviruses 19:625-629 (2003).
DR ENBL; AY214090; AAO61810.1; -; Genomic_RNA.
DR HSSP; P04624; 1JAU.
DR SMR; Q72UR9; 1-105.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Envelope protein.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14745 MW; 224464857307BFF9 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLEESQOQKNEQELLELDKWSLWNWF 36
DB 82 IYTLLEESQOQKNEQELLELDKWSLWNWF 113

RESULT 5
Q9EA82_9HIV1
ID Q9EA82_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q9EA82;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BX922;
RX MEDLINE=20134570; PubMed=106693328; DOI=10.1086/315253;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475 (2000).
DR ENBL; AF190970; AAG02332.1; -; Genomic_DNA.
DR HSSP; P31872; 1IB0.
DR SMR; Q9EA82; 1-105.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Envelope protein.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14804 MW; CF6AF2DC9EDA9C69 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLEESQOQKNEQELLELDKWSLWNWF 36
DB 82 IYTLLEESQOQKNEQELLELDKWSLWNWF 113

RESULT 6
Q9IUN5_9HIV1
ID Q9IUN5_9HIV1 PRELIMINARY; PRT; 122 AA.

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AC Q9IUN5;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AR36;
RX MEDLINE=20346416; PubMed=10890362; DOI=10.1089/08922220050058425;
RA Masciotra S., Livellara B., Bellosso W., Clara L., Tanuri A., Ramos A.,
RA Baggs J., Lal R., Pieniazek D.;
RT "Evidence for a high frequency of HIV-1 subtype F infections among
RT heterosexual population in Buenos Aires, Argentina.";
RL AIDS Res. Hum. Retroviruses 16:1007-1014 (2000).
DR ENBL; AF226697; AAF76816.1; -; Genomic_DNA.
DR HSSP; P12488; 1IM7.
DR SMR; Q9IUN5; 1-105.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Envelope protein.
FT NON_TER 1
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 14779 MW; C9B2C8944C48C614 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLEESQOQKNEQELLELDKWSLWNWF 36
DB 82 IYTLLEESQOQKNEQELLELDKWSLWNWF 113

RESULT 7
Q6V8Z2_9HIV1
ID Q6V8Z2_9HIV1 PRELIMINARY; PRT; 127 AA.
AC Q6V8Z2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yilmaz G., Midilli K., Turkoglu S., Kuskucu A.M., Bayraktaroglu Z.,
RA Aksoz A., Ozkan E., Calangu S., Altas K.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; AY347737; AAQ63672.1; -; Genomic_DNA.
DR SMR; Q6V8Z2; 1-107.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR Envelope protein.
FT NON_TER 1
FT NON_TER 127
FT NON_TER 127
SQ SEQUENCE 127 AA; 15450 MW; F775D7E19BF78A5B CRC64;

Query Match 88.9%; Score 32; DB 2; Length 127;
Best Local Similarity 100.0%; Pred. No. 2.4e-23;

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Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 IYTLLESQKQKNEQELLELDKWSLWNWF 36
Db 84 IYTLLESQKQKNEQELLELDKWSLWNWF 115

RESULT 8
Q6V8Y8_9HIV1
ID Q6V8Y8_9HIV1 PRELIMINARY; PRT; 141 AA.
AC Q6V8Y8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]_NUCLEOTIDE SEQUENCE.
RA Yilmaz G., Midilli K., Turkoglu S., Kuskucu A.M., Bayraktaroglu Z.,
RA Aksoezek A., Ozkan E., Calangu S., Altas K.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY347741; AAQ63676.1; -; Genomic_DNA.
DR SMR; Q6V8Y8; 3-82.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 141
FT NON_TER 141
SQ SEQUENCE 141 AA; 16814 MW; B6A0F119928C26A1 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.6e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 IYTLLESQKQKNEQELLELDKWSLWNWF 36
Db 98 IYTLLESQKQKNEQELLELDKWSLWNWF 129

RESULT 9
Q7ZC84_9HIV1
ID Q7ZC84_9HIV1 PRELIMINARY; PRT; 144 AA.
AC Q7ZC84;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]_NUCLEOTIDE SEQUENCE.
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with subtype B and non-B HIV-1 strains."
RL J. Acquir. Immune Defic. Syndr. 33:134-139(2003).
DR EMBL; AY18436; AAO65711.1; -; Genomic_RNA.
DR HSSP; Q89797; 1F23.
DR SMR; Q7ZC84; 11-98.
DR GO; GO:0016021; C:integral to membrane; IEA.
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 144
FT NON_TER 144
SQ SEQUENCE 144 AA; 16863 MW; AD6C57B998454949 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 IYTLLESQKQKNEQELLELDKWSLWNWF 36
Db 113 IYTLLESQKQKNEQELLELDKWSLWNWF 144

RESULT 10
Q7ZC84_9HIV1 PRELIMINARY; PRT; 144 AA.
ID Q7ZC84_9HIV1 PRELIMINARY; PRT; 144 AA.
AC Q7ZC84;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]_NUCLEOTIDE SEQUENCE.
RP MEDLINE=22679027; PubMed=12794544;
RX DOI=10.1097/00126334-200306010-00003;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in enfuvirtide-naive patients infected with subtype B and non-B HIV-1 strains."
RL J. Acquir. Immune Defic. Syndr. 33:134-139(2003).
DR EMBL; AY185376; AAO65651.1; -; Genomic_RNA.
DR HSSP; P12488; 1IM7.
DR SMR; Q7ZC84; 11-97.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 144
FT NON_TER 144
SQ SEQUENCE 144 AA; 16856 MW; 204A5328B6E248C CRC64;

Query Match 88.9%; Score 32; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.7e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 IYTLLESQKQKNEQELLELDKWSLWNWF 36
Db 113 IYTLLESQKQKNEQELLELDKWSLWNWF 144

RESULT 11
Q6YA57_9HIV1
ID Q6YA57_9HIV1 PRELIMINARY; PRT; 845 AA.
AC Q6YA57;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
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OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OX Lentivirus; Primate lentivirus group.  
ON NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CM237;  
RX MEDLINE=22866095; PubMed=14506784; DOI=10.1089/08922203322280937;  
RA Swanson P., Devare S.G., Hackett J. Jr.;  
RT "Full-length sequence analysis of HIV-1 isolate CM237: a CRF01\_AE/B  
inter-subtype recombinant from Thailand.";  
RL AIDS Res. Hum. Retroviruses 19:707-712(2003).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CM237;  
RA Swanson P.A., Devare S.G., Hackett J.R. Jr.;  
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY167123; AA040783.1; -; Genomic\_RNA.  
DR HSP; P04578; IK33.  
DR SMR; Q6YA57; 1-130, 100-348, 140-480, 529-615.  
DR GO; GO:0016021; C: integral to membrane; IEA.  
DR GO; GO:0019031; C: viral envelope; IEA.  
DR GO; GO:0005198; F: structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Envelope protein; Transmembrane.  
SQ SEQUENCE 845 AA; 95647 MW; 7A6654344CFD02AB CRC64;  
  
Query Match 88.9%; Score 32; DB 2; Length 845;  
Best Local Similarity 100.0%; Pred. No. 1.3e-22;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 5 IYTLLEESQKQKNEQELLELDKWSLWNWF 36  
DB 631 IYTLLEESQKQKNEQELLELDKWSLWNWF 662  
  
RESULT 12  
ENV HV1S3  
ID ENV HV1S3 STANDARD; PRT; 852 AA.  
AC P19549;  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane  
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].  
GN Name-ENV;  
OS Human immunodeficiency virus type 1 (isolate SF33) (HIV-1).  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11690;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=90317906; PubMed=2370688;  
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;  
RT "Human immunodeficiency virus type 1 cellular host range, replication,  
genome,";  
RL J. Virol. 64:4016-4020(1990).  
CC -----  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; AY352275; AAQ17031.1; -; Genomic\_DNA.  
DR PDB; 1MEQ; NMR; A=484-506.  
DR SMR; P19549; 536-622.  
DR HIV; M38427; ENV\$SF33.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.

DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW 3D-structure; AIDS; Capsid protein; Glycoprotein; Polyprotein; Signal;  
KW Structural protein; Transmembrane.  
FT SIGNAL 1 31 By similarity.  
FT CHAIN 32 506 Exterior membrane glycoprotein.  
FT CHAIN 507 852 Transmembrane glycoprotein.  
FT CARBOHYD 87 87 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 129 129 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 141 141 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 142 142 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 155 155 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 159 159 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 189 189 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 198 198 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 242 242 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 263 263 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 277 277 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 290 290 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 296 296 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 332 332 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 339 339 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 355 355 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 391 391 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 397 397 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 401 401 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 405 405 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 442 442 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 457 457 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 607 607 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 612 612 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 621 621 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 633 633 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 812 812 N-linked (GlcNAc...) (Potential).  
FT DISULFID 53 73 By similarity.  
FT DISULFID 118 206 By similarity.  
FT DISULFID 125 197 By similarity.  
FT DISULFID 130 156 By similarity.  
FT DISULFID 219 248 By similarity.  
FT DISULFID 229 240 By similarity.  
FT DISULFID 297 331 By similarity.  
FT DISULFID 377 439 By similarity.  
FT DISULFID 384 412 By similarity.  
SQ SEQUENCE 852 AA; 96663 MW; EE7BBF8D23C9910D CRC64;  
  
Query Match 88.9%; Score 32; DB 1; Length 852;  
Best Local Similarity 100.0%; Pred. No. 1.3e-22;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
OY 5 IYTLLEESQKQKNEQELLELDKWSLWNWF 36  
DB 638 IYTLLEESQKQKNEQELLELDKWSLWNWF 669  
  
RESULT 13  
ENV HV1S3  
ID ENV HV1S3 PRELIMINARY; PRT; 852 AA.  
AC P19549;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Envelope glycoprotein.  
GN Name-env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98178716; PubMed=9519894;  
RA McCutchan F.E., Sanders-Buell E., Salminen M.O., Carr J.K.,

RA Shepard W.H.;  
RT "Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in San Francisco Men's Health Study participants.";  
RL AIDS Res. Hum. Retroviruses 14:329-337(1998).  
DR EMBL; A025750; AAC40588.1; -; Genomic\_DNA.  
DR HSSP; P20871; 1CB4.  
DR SMR; 092761; 536-622.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Envelope protein; Transmembrane.  
SQ SEQUENCE 852 AA; 96544 MW; 3C7780DB0611E617 CRC64;  
  
Query Match 88.9%; Score 32; DB 2; Length 852;  
Best Local Similarity 100.0%; Pred. No. 1.3e-22;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 IYTLLEESQOQKNEQELLELDKWASLWNWF 36  
Db 638 IYTLLEESQOQKNEQELLELDKWASLWNWF 669  
  
RESULT 14  
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ID Q73303\_9HIV1 PRELIMINARY; PRT; 852 AA.  
AC Q73303;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein.  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=96263682; PubMed=8924250;  
RA Douglas N.W., Knight A.I., Hayhurst A., Barrett W.Y., Kevany M.J., Daniels R.S.;  
RT "An efficient method for the rescue and analysis of functional HIV-1 env genes: evidence for recombination in the vicinity of the tat/rev splice site.";  
RL AIDS 10:139-46(1996).  
DR EMBL; U36877; AAC55537.1; -; Genomic\_DNA.  
DR PIR; A53591; A53591.  
DR HSSP; P04578; 1DLB.  
DR SMR; Q73303; 81-125, 197-488, 536-622.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Envelope protein; Transmembrane.  
SQ SEQUENCE 852 AA; 96808 MW; A24BA64A133D149B CRC64;

Query Match 88.9%; Score 32; DB 2; Length 852;  
Best Local Similarity 100.0%; Pred. No. 1.3e-22;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IYTLLEESQOQKNEQELLELDKWASLWNWF 36  
Db 638 IYTLLEESQOQKNEQELLELDKWASLWNWF 669

RESULT 15  
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ID Q9E1R7\_9HIV1 PRELIMINARY; PRT; 855 AA.  
AC Q9E1R7;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope protein.  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20442410; PubMed=10984542; DOI=10.1073/pnas.97.19.10532;  
RA Cleghorn F.R., Jack N., Carr J.K., Edwards J., Mahabir B., Sill A., McDonald C.B., Connolly S.M., Goodman D., Bennetts R.Q., O'Brien T.R., Weinhold K.J., Bartholomew C., Blattner W.A., Greenberg M.L.;  
RT "A distinctive clade B HIV type 1 is heterosexually transmitted in Trinidad and Tobago.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:10532-10537(2000).  
DR EMBL; AF277071; AAG22514.1; -; Genomic\_DNA.  
DR HSSP; P31872; 1LB0.  
DR SMR; Q9E1R7; 539-625.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env GP41.  
DR InterPro; IPR000777; GP120.  
DR Pfam; PF00516; GP120; 1.  
DR Pfam; PF00517; GP41; 1.  
KW AIDS; Envelope protein; Transmembrane.  
SQ SEQUENCE 855 AA; 97102 MW; 26271D6CCCCCFFAC CRC64;  
  
Query Match 88.9%; Score 32; DB 2; Length 855;  
Best Local Similarity 100.0%; Pred. No. 1.3e-22;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 5 IYTLLEESQOQKNEQELLELDKWASLWNWF 36  
Db 641 IYTLLEESQOQKNEQELLELDKWASLWNWF 672  
  
Search completed: March 6, 2006, 16:25:16  
Job time : 123 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:25:38 ; Search time 28.6667 Seconds  
(without alignments)  
103.825 Million cell updates/sec

Title: US-09-809-060A-2

Perfect score: 36

Sequence: 1 YNTIYTLLESQKQKNEQELLELDKWLNNWF 36

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/prodata/1/iaa/5\_COMB.pep.\*
- 2: /cgn2\_6/prodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/prodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep.\*
- 5: /cgn2\_6/prodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	36	2 US-08-486-099-3	Sequence 3, Appli
2	36	100.0	36	2 US-08-484-223B-3	Sequence 3, Appli
3	36	100.0	36	2 US-08-319-597-3	Sequence 3, Appli
4	36	100.0	36	2 US-08-475-668A-3	Sequence 3, Appli
5	36	100.0	36	2 US-08-485-551A-3	Sequence 3, Appli
6	36	100.0	36	2 US-08-471-913A-3	Sequence 3, Appli
7	36	100.0	36	2 US-08-485-264A-3	Sequence 3, Appli
8	36	100.0	36	2 US-09-082-279B-1357	Sequence 1357, Ap
9	36	100.0	36	2 US-08-474-349A-3	Sequence 3, Appli
10	36	100.0	36	2 US-09-315-304B-1357	Sequence 1357, Ap
11	36	100.0	36	2 US-08-255-208A-3	Sequence 3, Appli
12	36	100.0	36	2 US-08-973-952-3	Sequence 3, Appli
13	36	100.0	36	2 US-08-470-896-3	Sequence 3, Appli
14	36	100.0	36	2 US-08-485-546A-3	Sequence 3, Appli
15	36	100.0	36	2 US-09-834-784-1357	Sequence 1357, Ap
16	36	100.0	36	2 US-09-515-965A-1357	Sequence 1357, Ap
17	36	100.0	36	2 US-09-350-641C-1357	Sequence 1357, Ap
18	36	100.0	36	2 US-09-350-841A-1357	Sequence 1357, Ap
19	36	100.0	36	2 US-08-487-266A-3	Sequence 3, Appli
20	36	100.0	36	2 US-09-623-548A-1421	Sequence 1421, Ap
21	36	100.0	36	2 US-10-252-136-3	Sequence 3, Appli
22	36	100.0	36	2 US-09-657-276-1421	Sequence 1421, Ap
23	36	100.0	36	2 US-08-484-741-3	Sequence 3, Appli
24	36	100.0	138	2 US-09-570-921-16	Sequence 16, Appli
25	36	100.0	145	1 US-08-394-021-11	Sequence 11, Appli
26	36	100.0	145	2 US-09-131-551-11	Sequence 11, Appli
27	36	100.0	145	2 US-10-000-321-11	Sequence 11, Appli

Query Match 100.0%; Score 36; DB 2; Length 36;

28 36 100.0 269 2 US-08-965-056-30 Sequence 30, Appli  
29 36 100.0 269 2 US-08-965-056-31 Sequence 31, Appli  
30 36 100.0 610 2 US-09-257-490-12 Sequence 12, Appli  
31 36 100.0 855 2 US-07-956-483-15 Sequence 15, Appli  
32 36 100.0 887 2 US-08-472-240A-6 Sequence 6, Appli  
33 32 88.9 36 2 US-09-082-279B-856 Sequence 856, App  
34 32 88.9 36 2 US-09-315-304B-856 Sequence 856, App  
35 32 88.9 36 2 US-09-834-784-856 Sequence 856, App  
36 32 88.9 36 2 US-09-515-965A-856 Sequence 856, App  
37 32 88.9 36 2 US-09-350-641C-856 Sequence 856, App  
38 32 88.9 36 2 US-09-350-841A-856 Sequence 19, Appli  
39 32 88.9 138 2 US-09-570-921-19 Sequence 19, Appli  
40 32 88.9 269 2 US-08-965-056-28 Sequence 28, Appli  
41 29 80.6 36 1 US-08-073-028-3 Sequence 3, Appli  
42 29 80.6 36 2 US-08-360-107A-3 Sequence 3, Appli  
43 29 80.6 36 2 US-08-554-616-3 Sequence 3, Appli  
44 29 80.6 36 2 US-09-082-279B-1051 Sequence 1051, Ap  
45 29 80.6 36 2 US-09-315-304B-1051 Sequence 1051, Ap

#### ALIGNMENTS

#### RESULT 1

US-08-486-099-3  
; Sequence 3, Application US/08486099  
; Patent No. 6013263

; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS

; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,099  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-031  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown

; MOLECULE TYPE: peptide  
US-08-486-099-3

Best Local Similarity 100.0%; Pred. No. 2.8e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36  
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

## RESULT 2

US-08-484-223B-3  
; Sequence 3, Application US/08484223B  
; Patent No. 6020459  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 245  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,223B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-029  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide

US-08-484-223B-3

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36  
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

## RESULT 3

US-08-919-597-3  
; Sequence 3, Application US/08919597  
; Patent No. 6054265  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 273  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/919,597  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/470,896  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-020  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide

US-08-919-597-3

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36  
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

## RESULT 4

US-08-475-669A-3  
; Sequence 3, Application US/08475668A  
; Patent No. 606065  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 211  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711



QY 1 YNTYITVLLSESONQEKNEQELLELDKWASLWNWF 36  
Db 1 YNTYITVLLSESONQEKNEQELLELDKWASLWNWF 36

## RESULT 7

US-08-485-264A-3  
; Sequence 3, Application US/08485264A  
; Patent No. 6228983  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,264A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-021  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-485-264A-3

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITVLLSESONQEKNEQELLELDKWASLWNWF 36  
Db 1 YNTYITVLLSESONQEKNEQELLELDKWASLWNWF 36

## RESULT 8

US-09-082-279B-1357  
; Sequence 1357, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anyer, Mohmed  
; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082,279B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1357  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-082-279B-1357

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITVLLSESONQEKNEQELLELDKWASLWNWF 36  
Db 1 YNTYITVLLSESONQEKNEQELLELDKWASLWNWF 36

## RESULT 9

US-08-474-349A-3  
; Sequence 3, Application US/08474349A  
; Patent No. 6333395  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA  
; NUMBER OF SEQUENCES: 517  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,349A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-474-349A-3

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36  
Db 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36

## RESULT 10.

US-09-315-304B-1357  
Sequence 1357, Application US/09315304B  
Patent No. 6348568  
GENERAL INFORMATION:  
APPLICANT: Barney, S.  
APPLICANT: Guthrie, K.  
APPLICANT: Merutka, G.  
APPLICANT: Anwer, M.  
APPLICANT: Lambert, D.  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
TITLE OF INVENTION: PROPERTIES  
FILE REFERENCE: 7872-052  
CURRENT APPLICATION NUMBER: US/09/315,304B  
CURRENT FILING DATE: 1999-05-20  
PRIOR APPLICATION NUMBER: 09/082,279  
PRIOR FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1667  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1357  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1357

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36  
Db 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36

## RESULT 11

US-08-255-208A-3  
Sequence 3, Application US/08255208A  
Patent No. 6440656  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway Jr., Stephen R.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/255,208A

FILING DATE: 07-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-255-208A-3

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36  
Db 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36

## RESULT 12

US-08-973-952-3  
Sequence 3, Application US/08973952A  
Patent No. 6475491  
GENERAL INFORMATION:  
APPLICANT: Johnson, M. Ross  
APPLICANT: Lambert, Dennis M.  
TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS  
TITLE OF INVENTION: USING COMBINATORY THERAPY  
FILE REFERENCE: 7872-036  
CURRENT APPLICATION NUMBER: US/08/973,952A  
CURRENT FILING DATE: 1998-05-29  
EARLIER APPLICATION NUMBER: 08/481,957  
EARLIER FILING DATE: 1995-06-07  
NUMBER OF SEQ ID NOS: 82  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus  
US-08-973-952-3

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36  
Db 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36

## RESULT 13

US-08-470-896-3  
Sequence 3, Application US/08470896  
Patent No. 6479055  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION

```
;
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-470-896-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 14
US-08-485-546A-3
; Sequence 3, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
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; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-485-546A-3

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 15
US-09-834-784-1357
; Sequence 1357, Application US/09834784
; Patent No. 6562787
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohmed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/834,784
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1357
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-834-784-1357

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36
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Search completed: March 6, 2006, 16:27:50  
Job time : 28.6667 secs





A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70421  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-140,'X',142-312,'X',314-357 <STE2>  
A:Cross-references: UNIPARC:UPI00000PF05F; EMBL:X61355; NID:g60179  
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.0%; Score 27; DB 2; Length 357;  
Best Local Similarity 100.0%; Pred. No. 2.8e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWSLWNWF 36  
DB 148 EESQNOEKNEQELLELDKWSLWNWF 174

RESULT 3  
S21996  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S70422; S21996  
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A>Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A:Reference number: S70417; MUID:92144209; PMID:1736940  
A:Accession: S70422  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-357 <ST2>  
A:Cross-references: UNIPROT:Q78119; UNIPARC:UPI0000104EC6; EMBL:X61356; NID:g60181; PIDN:1736940  
A:Experimental source: patient 27L  
A>Note: submitted to the EMBL Data Library, July 1991  
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.0%; Score 27; DB 2; Length 357;  
Best Local Similarity 100.0%; Pred. No. 2.8e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWSLWNWF 36  
DB 148 EESQNOEKNEQELLELDKWSLWNWF 174

RESULT 4  
C41621  
env polyprotein P - human immunodeficiency virus type 1 (fragment)  
N:Alternate names: coat polyprotein  
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Accession: C41621  
C>Date: 11-Feb-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.  
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991  
A>Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity  
A:Reference number: A41621; MUID:92107924; PMID:1763038  
A:Accession: C41621  
A:Molecule type: DNA  
A:Residues: 1-443 <BP>  
A:Cross-references: UNIPROT:Q80023; UNIPARC:UPI0000104256; GB:M77230; NID:g328631; PIDN:1763038  
A>Note: this virus was isolated from the mother's sexual partner  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP>  
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP>  
F:424-443/Domain: transmembrane #status predicted <TM>  
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,377/Binding site: ca

Query Match 75.0%; Score 27; DB 2; Length 443;  
Best Local Similarity 100.0%; Pred. No. 3.5e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWSLWNWF 36  
DB 387 EESQNOEKNEQELLELDKWSLWNWF 413

RESULT 5  
T09448  
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T09448  
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie, submitted to the EMBL Data Library, July 1996  
A:Reference number: Z16673  
A:Accession: T09448  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-847 <PAN>  
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI000010C516; EMBL:U63632; NID:g1465777; PII:16673  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.0%; Score 27; DB 2; Length 847;  
Best Local Similarity 100.0%; Pred. No. 6.4e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWSLWNWF 36  
DB 638 EESQNOEKNEQELLELDKWSLWNWF 664

RESULT 6  
S13289  
env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S13289  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Digne, A.; Idler, K.; Zack, J.A.  
Nature 348, 69-73, 1990  
A>Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13289  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-847 <OBR>  
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI000017861B  
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.0%; Score 27; DB 2; Length 847;  
Best Local Similarity 100.0%; Pred. No. 6.4e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOEKNEQELLELDKWSLWNWF 36  
DB 638 EESQNOEKNEQELLELDKWSLWNWF 664

RESULT 7  
S33985  
env polyprotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S33985  
R:Carlini, F.  
submitted to the EMBL Data Library, November 1991  
A:Reference number: S33979  
A:Accession: S33985  
A>Status: preliminary

A:Molecule type: mRNA  
A:Residues: 1-851 <CAR>  
A:Cross-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:Z11530; NID:g60192; PIDN  
C:Superfamily: type E retrovirus env polyprotein

Query Match 75.0%; Score 27; DB 2; Length 851;  
Best Local Similarity 100.0%; Pred. No. 6.4e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEQELLELDKWSLWNNF 36  
Db 642 EESONQOEKNEQELLELDKWSLWNNF 668

RESULT 8  
S13288  
env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Dec-2004  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.  
Nature 348, 69-73, 1990  
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OBR>  
A:Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:Q90178; UNIPROT:Q78243; UNIP

Query Match 75.0%; Score 27; DB 2; Length 854;  
Best Local Similarity 100.0%; Pred. No. 6.4e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEQELLELDKWSLWNNF 36  
Db 645 EESONQOEKNEQELLELDKWSLWNNF 671

RESULT 9  
VCLJ3W  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C:Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 09-Jul-2004  
C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
Cell 45, 637-648, 1986  
A:Title: Identification and characterization of conserved and variable regions in the en  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774  
A:Molecule type: DNA  
A:Residues: 1-856 <STA>  
A:Cross-references: UNIPROT:P31872; UNIPARC:UPI000012A024; GB:K03455; GB:M38432; NID:glu  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-501/Product: coat protein gp120 #status predicted <GP1>  
F:502-847/Product: coat protein gp41 #status predicted <GP2>  
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459

Query Match 75.0%; Score 27; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 6.4e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEQELLELDKWSLWNNF 36  
Db 647 EESONQOEKNEQELLELDKWSLWNNF 673

RESULT 10  
VCLJTV  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1

VCLJTH3  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C:Accession: A03973  
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doraz  
nberger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.  
Nature 313, 277-284, 1985  
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.  
A:Reference number: A93353; MUID:85111123; PMID:2578615  
A:Accession: A03973  
A:Molecule type: DNA  
A:Residues: 1-856 <RAT>  
A:Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K020  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,155,160,186,197,230,234,241,262,276,289,295,301,312,339,356,386,392,397,406;  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict  
Query Match 75.0%; Score 27; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 6.4e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEQELLELDKWSLWNNF 36  
Db 647 EESONQOEKNEQELLELDKWSLWNNF 673

RESULT 11  
VCLJSC  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C:Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C:Accession: B28922  
R:Guo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta  
Virology 164, 531-536, 1988  
A:Title: Envelope sequences of two new United States HIV-1 isolates.  
A:Reference number: A28922; MUID:88219542; PMID:3369091  
A:Accession: B28922  
A:Molecule type: DNA  
A:Residues: 1-861 <GUR>  
A:Cross-references: UNIPARC:UPI0000174A39  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protei  
F:1-29/Domain: signal sequence #status predicted <SIG>  
F:30-861/Product: env polyprotein #status predicted <EPP>  
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396,  
Query Match 75.0%; Score 27; DB 1; Length 861;  
Best Local Similarity 100.0%; Pred. No. 6.5e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESONQOEKNEQELLELDKWSLWNNF 36  
Db 652 EESONQOEKNEQELLELDKWSLWNNF 678

RESULT 12  
VCLJLV  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1

A;Title: host Homo sapiens (man)  
C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C;Accession: A03975  
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A;Title: Nucleotide sequence of the AIDS virus, LAV.  
A;Reference number: A90866; MUID:8509333; PMID:2981635  
A;Accession: A03975  
A;Molecule type: DNA  
A;Residues: 1-861 <WAI>  
A;Cross-references: UNIPROT:P03377; UNIPARC:UPI000012A013; GB:X02013; NID:g326417; PIDN:  
C;Genetics:  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>  
F;517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411  
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 75.0%; Score 27; DB 1; Length 861;  
Best Local Similarity 100.0%; Pred. No. 6.5e-19;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 10 EESQOQEKNEQELLELDKWASLWNWF 36  
Db 652 EESQOQEKNEQELLELDKWASLWNWF 678  
RESULT 13  
S21998  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Variety: isolate 28  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S21998; S70425  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined  
A;Reference number: S21998  
A;Accession: S21998  
A;Molecule type: DNA  
A;Residues: 1-358 <STEL>  
A;Cross-references: UNIPROT:Q78120; UNIPARC:UPI0000178607; EMBL:X61359; NID:g60182; PIDN:  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal  
A;Reference number: S70417; MUID:92144209; PMID:1736940  
A;Accession: S70425  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-222,'X',224-358 <STE2>  
A;Cross-references: UNIPARC:UPI00000FE72C; EMBL:X61359; NID:g60182; PIDN:CAA43630.1; PIDN:  
C;Superfamily: type E retrovirus env polyprotein  
Query Match 69.4%; Score 25; DB 2; Length 358;  
Best Local Similarity 100.0%; Pred. No. 2.7e-17;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 SQOQEKNEQELLELDKWASLWNWF 36  
Db 151 SQOQEKNEQELLELDKWASLWNWF 175  
RESULT 14  
S21992  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S70424; S21992  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal  
A;Reference number: S70417; MUID:92144209; PMID:1736940  
A;Accession: S70424  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-357 <ST2>  
A;Cross-references: UNIPROT:Q78112; UNIPARC:UPI0000107A48; EMBL:X61358; NID:g60177; PIDN:  
A;Experimental source: patient 22  
A;Note: submitted to the EMBL Data Library, July 1991  
C;Superfamily: type E retrovirus env polyprotein  
Query Match 61.1%; Score 22; DB 2; Length 357;  
Best Local Similarity 100.0%; Pred. No. 2.5e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 12 SQOQEKNEQELLELDKWASLW 33  
Db 150 SQOQEKNEQELLELDKWASLW 171  
RESULT 15  
S54384  
envelope polyprotein - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C;Accession: S54384  
R;Theodore, T.; Buckler-White, A.J.  
submitted to the EMBL Data Library, July 1989  
A;Reference number: S54377  
A;Accession: S54384  
A;Status: preliminary  
A;Molecule type: genomic RNA  
A;Residues: 1-853 <THE>  
A;Cross-references: UNIPROT:P12487; UNIPARC:UPI000012A027; EMBL:M22639; NID:g329377; PIDN:  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: polyprotein  
Query Match 61.1%; Score 22; DB 2; Length 853;  
Best Local Similarity 100.0%; Pred. No. 5.5e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 QOQEKNEQELLELDKWASLWNWF 36  
Db 649 QOQEKNEQELLELDKWASLWNWF 670  
Search completed: March 6, 2006, 16:26:19  
Job time : 20 secs



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;
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-3

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLESQKQKNEQELLELDKWASLWNWF 36

RESULT 3
US-10-351-641-1357
; Sequence 1357, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1357
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1357

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLESQKQKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLESQKQKNEQELLELDKWASLWNWF 36

RESULT 4
US-10-267-682-3
; Sequence 3, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
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; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-267-748-3

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKQASLWNWF 36
DB 1 YNTIYTLLESQKQKNEQELLELDKQASLWNWF 36

RESULT 6
US-10-663-589-38
; Sequence 38, Application US/10663589
; Publication No. US20040063637A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-38

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKQASLWNWF 36
DB 1 YNTIYTLLESQKQKNEQELLELDKQASLWNWF 36

RESULT 7
US-10-671-282-38
; Sequence 38, Application US/10671282
; Publication No. US20040122214A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
; TITLE OF INVENTION: their use in therapy
; FILE REFERENCE: TRM-004

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; CURRENT APPLICATION NUMBER: US/10/671,282
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/414,439
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-671-282-38

Query Match 100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKQASLWNWF 36
DB 1 YNTIYTLLESQKQKNEQELLELDKQASLWNWF 36

RESULT 8
US-10-168-295-3
; Sequence 3, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Baroudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-3

Query Match 100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 9.1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKQASLWNWF 36
DB 1 YNTIYTLLESQKQKNEQELLELDKQASLWNWF 36

RESULT 9
US-10-950-010-3
; Sequence 3, Application US/10950010
; Publication No. US20050070475A1
; GENERAL INFORMATION:
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: DUFRESNE, Robert S.
; APPLICANT: BOUDJELLAB, Nissab
; APPLICANT: ROBITAILLE, Martin
; APPLICANT: MILNER, Peter G.
; TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL
; TITLE OF INVENTION: INFECTION
; FILE REFERENCE: 500862001501/REDC-1512
; CURRENT APPLICATION NUMBER: US/10/950,010
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: US 09/623,533
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13651
; PRIOR FILING DATE: 2000-05-17

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/000,321
; FILING DATE: 04-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/131,551
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: SANDERCOCK, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 58315/106/BEAK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-000-321-11
Query Match 100.0%; Score 36; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 3e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWP 36
Db 106 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWP 141
RESULT 13
US-09-854-816-30
; Sequence 30, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovashnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-854-816-31
Query Match 100.0%; Score 36; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.2e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWP 36
Db 169 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWP 204
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;
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-854-816-30
Query Match 100.0%; Score 36; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.2e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWP 36
Db 169 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWP 204
RESULT 14
US-09-854-816-31
; Sequence 31, Application US/09854816
; Patent No. US20020151473A1
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; J. Kevin Judice
; Robert S. McDowell
; J. Christopher Phelan
; Melissa A. Starovashnik
; James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; Making Same
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/854,816
; FILING DATE: 15-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/965,056
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Ph.D., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-854-816-31
Query Match 100.0%; Score 36; DB 3; Length 269;
Best Local Similarity 100.0%; Pred. No. 5.2e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWP 36
Db 169 YNTNTYTLLESQNOQEKNEQELLELDKWASLWNWP 204
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RESULT 15  
US-10-351-641-856  
; Sequence 856, Application US/10351641  
; Publication No. US20030186874A1  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-100  
; CURRENT APPLICATION NUMBER: US/10/351,641  
; CURRENT FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 09/350,641  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/315,304  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1757  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 856  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-10-351-641-856

Query Match 88.9%; Score 32; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 5.4e-23;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 IYTLLEESQNKQEKNEQELLELDKWSLWNWF 36  
Db 5 IYTLLEESQNKQEKNEQELLELDKWSLWNWF 36

Search completed: March 6, 2006, 16:32:48  
Job time : 97.3333 secs



US-11-084-858-11

Query Match 75.0%; Score 36; DB 7; Length 145;  
Best Local Similarity 100.0%; Pred. No. 4.6e-29;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTNITVTLLESQKQKNEQELLELDKWSLWVNF 36  
|||||  
DB 106 YTNITVTLLESQKQKNEQELLELDKWSLWVNF 141

RESULT 2

US-10-841-956A-1  
; Sequence 1, Application US/10841956A  
; Publication No. US20050281829A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN HEHIR, CRISTINA A.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: STATTEL, JAMES M.  
; APPLICANT: PALOMBELLA, VITO J.  
; APPLICANT: BITONTI, ALAN R.  
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS  
; FILE REFERENCE: 08945.0003-00000  
; CURRENT APPLICATION NUMBER: US/10/841.956A  
; PRIOR FILING DATE: 2004-05-06  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-841-956A-1

Query Match 75.0%; Score 27; DB 6; Length 36;  
Best Local Similarity 100.0%; Pred. No. 9.7e-21;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKQKNEQELLELDKWSLWVNF 36  
|||||  
DB 10 EESQKQKNEQELLELDKWSLWVNF 36

RESULT 3

US-11-029-003-1  
; Sequence 1, Application US/11029003  
; Publication No. US20050260194A1  
; GENERAL INFORMATION:  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: RIVERA, DANIEL S.  
; APPLICANT: BITONTI, ALAN J.  
; APPLICANT: STATTEL, JAMES  
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS  
; FILE REFERENCE: 08945.0007-01000  
; CURRENT APPLICATION NUMBER: US/11/029.003  
; PRIOR FILING DATE: 2005-01-05  
; PRIOR APPLICATION NUMBER: 60/539,207  
; PRIOR FILING DATE: 2004-01-26  
; PRIOR APPLICATION NUMBER: 60/487,964  
; PRIOR FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: 60/469,600  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-11-029-003-1

Query Match 75.0%; Score 27; DB 7; Length 36;  
Best Local Similarity 100.0%; Pred. No. 9.7e-21;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKQKNEQELLELDKWSLWVNF 36  
|||||  
DB 10 EESQKQKNEQELLELDKWSLWVNF 36

RESULT 4

US-11-187-687-22  
; Sequence 22, Application US/11187687  
; Publication No. US20060019347A1  
; GENERAL INFORMATION:  
; APPLICANT: Cho, Ho Sung  
; APPLICANT: Daniel, Thomas O.  
; APPLICANT: Hays, Anna-Maria  
; APPLICANT: Wilson, Troy E.  
; APPLICANT: Litzinger, David C.  
; APPLICANT: Mariani, Roberto  
; APPLICANT: Kimmel, Bruce E.  
; APPLICANT: Keefe, William M.  
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino  
; TITLE OF INVENTION: Acids  
; FILE REFERENCE: AMBX-0041.00US  
; CURRENT APPLICATION NUMBER: US/11/187,687  
; PRIOR FILING DATE: 2005-07-21  
; PRIOR FILING DATE: 2004-07-21  
; PRIOR APPLICATION NUMBER: 60/590,035  
; PRIOR FILING DATE: 2005-03-07  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 22  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-11-187-687-22

Query Match 75.0%; Score 27; DB 7; Length 36;  
Best Local Similarity 100.0%; Pred. No. 9.7e-21;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKQKNEQELLELDKWSLWVNF 36  
|||||  
DB 10 EESQKQKNEQELLELDKWSLWVNF 36

RESULT 5

US-11-112-277-33  
; Sequence 33, Application US/11112277  
; Publication No. US20050267293A1  
; GENERAL INFORMATION:  
; APPLICANT: Bousquet-Gagnon, Nathalie  
; APPLICANT: Quraishi, Omar  
; APPLICANT: Bridon, Dominique P.  
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN  
; FILE REFERENCE: 500862003700  
; CURRENT APPLICATION NUMBER: US/11/112,277  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/565,228  
; PRIOR FILING DATE: 2004-04-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: T20 Analogue  
; FEATURE:  
; NAME/KEY: MOD\_RES

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; LOCATION: 37
; OTHER INFORMATION: Xaa is Lys linked to AREA-MEA
US-11-112-277-33

Query Match      75.0%; Score 27; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 9.9e-21;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESNQOQEKNEQELLELDKQASLWNNWF 36
Db 10 EESNQOQEKNEQELLELDKQASLWNNWF 36

RESULT 6
US-11-089-426-10
; Sequence 10, Application US/11089426
; Publication No. US20050261229A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Wesolowski, John
; TITLE OF INVENTION: Fc Fusion Proteins For Enhancing the Immunogenicity of
; TITLE OF INVENTION: Protein and Peptide Antigens
; FILE REFERENCE: LEX-007
; CURRENT APPLICATION NUMBER: US/11/089,426
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US/09/621,268
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/144,965
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fused
; OTHER INFORMATION: polypeptide from pDC-muFC vector
US-11-089-426-10

Query Match      75.0%; Score 27; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESNQOQEKNEQELLELDKQASLWNNWF 36
Db 8 EESNQOQEKNEQELLELDKQASLWNNWF 34

RESULT 7
US-11-187-687-24
; Sequence 24, Application US/11187687
; Publication No. US20060019347A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Ho Sung
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Hays, Anna-Maria
; APPLICANT: Wilson, Troy E.
; APPLICANT: Litzynger, David C.
; APPLICANT: Mariani, Roberto
; APPLICANT: Kimmel, Bruce E.
; APPLICANT: Keefe, William M.
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
; FILE REFERENCE: AMEX-0041.0005
; CURRENT APPLICATION NUMBER: US/11/187,687
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: 60/590,035
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: 60/659,709
; PRIOR FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 28
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-24

Query Match      75.0%; Score 27; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESNQOQEKNEQELLELDKQASLWNNWF 36
Db 18 EESNQOQEKNEQELLELDKQASLWNNWF 44

RESULT 8
US-10-841-956A-4
; Sequence 4, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-841-956A-4

Query Match      75.0%; Score 27; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 6.6e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESNQOQEKNEQELLELDKQASLWNNWF 36
Db 241 EESNQOQEKNEQELLELDKQASLWNNWF 267

RESULT 9
US-10-841-956A-8
; Sequence 8, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
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; LENGTH: 269  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Peptide  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: construct  
US-10-841-956A-8

Query Match 75.0%; Score 27; DB 6; Length 269;  
Best Local Similarity 100.0%; Pred. No. 6.7e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWSLWNWF 36  
|||  
Db 243 EESQOQEKNEQELLELDKWSLWNWF 269

## RESULT 10

US-10-841-956A-5  
; Sequence 5, Application US/10841956A  
; Publication No. US20050281829A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN HEHIR, CRISTINA A.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: STATTEL, JAMES M.  
; APPLICANT: PALOMBELLA, VITO J.  
; APPLICANT: BITONTI, ALAN R.  
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS  
; FILE REFERENCE: 08945.0003-00000  
; CURRENT APPLICATION NUMBER: US/10/841,956A  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: 60/468,835  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 5  
; LENGTH: 270  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Peptide  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-841-956A-5

Query Match 75.0%; Score 27; DB 6; Length 270;  
Best Local Similarity 100.0%; Pred. No. 6.7e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWSLWNWF 36  
|||  
Db 10 EESQOQEKNEQELLELDKWSLWNWF 36

## RESULT 11

US-10-841-956A-7  
; Sequence 7, Application US/10841956A  
; Publication No. US20050281829A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN HEHIR, CRISTINA A.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: STATTEL, JAMES M.  
; APPLICANT: PALOMBELLA, VITO J.  
; APPLICANT: BITONTI, ALAN R.  
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS  
; FILE REFERENCE: 08945.0003-00000  
; CURRENT APPLICATION NUMBER: US/10/841,956A  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: 60/468,835  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 7  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Peptide  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: construct  
US-10-841-956A-7

Query Match 75.0%; Score 27; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 7e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWSLWNWF 36  
|||  
Db 10 EESQOQEKNEQELLELDKWSLWNWF 36

## RESULT 12

US-10-841-956A-6  
; Sequence 6, Application US/10841956A  
; Publication No. US20050281829A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN HEHIR, CRISTINA A.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: STATTEL, JAMES M.  
; APPLICANT: PALOMBELLA, VITO J.  
; APPLICANT: BITONTI, ALAN R.  
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS  
; FILE REFERENCE: 08945.0003-00000  
; CURRENT APPLICATION NUMBER: US/10/841,956A  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: 60/468,835  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 6  
; LENGTH: 282  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Peptide  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-841-956A-6

Query Match 75.0%; Score 27; DB 6; Length 282;  
Best Local Similarity 100.0%; Pred. No. 7e-20;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWSLWNWF 36  
|||  
Db 256 EESQOQEKNEQELLELDKWSLWNWF 282

## RESULT 13

US-10-841-956A-9  
; Sequence 9, Application US/10841956A  
; Publication No. US20050281829A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN HEHIR, CRISTINA A.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: STATTEL, JAMES M.  
; APPLICANT: PALOMBELLA, VITO J.  
; APPLICANT: BITONTI, ALAN R.  
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS  
; FILE REFERENCE: 08945.0003-00000  
; CURRENT APPLICATION NUMBER: US/10/841,956A  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: 60/468,835  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 59

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 9

; LENGTH: 293

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE: Peptide

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: construct

US-10-841-956A-9

Query Match

Best Local Similarity 75.0%; Score 27; DB 6; Length 293;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWASLWNWF 36

Db 267 EESQNOQEKNEQELLELDKWASLWNWF 293

RESULT 14

US-11-053-100-27

; Sequence 27, Application US/11053100

; Publication No. US2005025554A1

; GENERAL INFORMATION:

; APPLICANT: CHILKOTI, Ashutosh

; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION

; FILE REFERENCE: 4176-101 CIP

; CURRENT APPLICATION NUMBER: US/11/053,100

; CURRENT FILING DATE: 2005-02-08

; PRIOR APPLICATION NUMBER: US 09/812,382

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 60/190,659

; PRIOR FILING DATE: 2000-03-20

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 27

; LENGTH: 354

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)..(354)

; OTHER INFORMATION: pET15b-ELP4-60-EK-T20 peptide

US-11-053-100-27

Query Match

Best Local Similarity 75.0%; Score 27; DB 7; Length 354;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWASLWNWF 36

Db 328 EESQNOQEKNEQELLELDKWASLWNWF 354

RESULT 15

US-11-053-100-36

; Sequence 36, Application US/11053100

; Publication No. US2005025554A1

; GENERAL INFORMATION:

; APPLICANT: CHILKOTI, Ashutosh

; TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION

; FILE REFERENCE: 4176-101 CIP

; CURRENT APPLICATION NUMBER: US/11/053,100

; CURRENT FILING DATE: 2005-02-08

; PRIOR APPLICATION NUMBER: US 09/812,382

; PRIOR FILING DATE: 2001-03-20

; PRIOR APPLICATION NUMBER: US 60/190,659

; PRIOR FILING DATE: 2000-03-20

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 36

; LENGTH: 356

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)..(356)

; OTHER INFORMATION: pET17b-ELP4-60-TEV(Q/Y)-T20 peptide

US-11-053-100-36

Query Match

Best Local Similarity 75.0%; Score 27; DB 7; Length 356;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWASLWNWF 36

Db 330 EESQNOQEKNEQELLELDKWASLWNWF 356

Search completed: March 6, 2006, 16:33:25

Job time : 10.3333 secs

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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:12:57 ; Search time 117.333 Seconds  
(without alignments)  
134.809 Million cell updates/sec

Title: US-09-809-060A-2  
Perfect score: 36  
Sequence: 1 YTWIITLLESQKQKNEQELLELDKWASLWNP 36

Scoring table: OLIGO  
Gap 60.0, Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: A\_Geneseq\_21.\*  
2: Geneseq1980s.\*  
3: Geneseq1990s.\*  
4: Geneseq2000s.\*  
5: Geneseq2001s.\*  
6: Geneseq2002s.\*  
7: Geneseq2003s.\*  
8: Geneseq2004s.\*  
9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	36	3 AAY89837	Core poly
2	36	100.0	36	4 AAB54786	HIV antiv
3	36	100.0	36	4 AAB92245	Virus rel
4	36	100.0	36	4 AAB78238	Core poly
5	36	100.0	36	4 AAB78237	Core poly
6	36	100.0	36	4 AAU70180	HIV viral
7	36	100.0	36	4 ABB02830	Viral cor
8	36	100.0	36	4 ABB01245	Viral DP1
9	36	100.0	36	4 ABB01244	Viral DP1
10	36	100.0	36	4 AAU13791	DP178-lik
11	36	100.0	36	4 AAU13790	DP178-lik
12	36	100.0	36	5 AAU18772	HIV gp41
13	36	100.0	36	5 ADE02850	Hybrid po
14	36	100.0	36	5 ADE02716	Hybrid po
15	36	100.0	36	6 ABO10164	HIV1-SF2
16	36	100.0	36	8 ADN06923	Peptide #
17	36	100.0	36	8 ADS87258	HIV1 gp4
18	36	100.0	36	9 AAY71493	HIV-1 tra
19	36	100.0	269	2 AAY22835	SEQ ID NO
20	36	100.0	269	2 AAY22834	SEQ ID NO
21	36	100.0	269	5 ABG68305	Envelope
22	36	100.0	269	5 ABG68306	Envelope
23	36	100.0	269	6 ABUS5712	Human imm
24	36	100.0	269	6 ABUS5713	Human imm

25	36	100.0	275	2 AAW33615	SOD/env-5
26	36	100.0	275	3 AAY77309	HIV-1 env
27	36	100.0	275	6 ABUS7560	AIDS asso
28	36	100.0	275	6 ABUG3193	Amino aci
29	36	100.0	700	2 AAR05795	HIV-1 env
30	36	100.0	855	2 AAW53112	ENV prote
31	36	100.0	855	3 AAY77298	HIV-1 (AT
32	36	100.0	855	3 AAY77302	HIV-1 (AT
33	36	100.0	855	6 ABUS7553	AIDS asso
34	36	100.0	855	6 ABUS7550	AIDS asso
35	36	100.0	855	6 ABUG3182	Protein #
36	36	100.0	855	6 ABUG3186	Env prote
37	36	100.0	855	8 ADO26144	HIV env p
38	36	100.0	855	9 ADX39689	HIV env p
39	36	100.0	860	2 AAW31284	HIV-SF2 v
40	36	100.0	863	1 AAP61509	Sequence
41	36	100.0	863	2 AAR29706	env gene
42	36	100.0	863	5 AAE35790	ARV-2 (9B
43	35	97.2	842	8 ADM73868	HIV-1 pol
44	33	91.7	854	2 AAW43070	HIV-1 gp1
45	32	88.9	36	3 AAY89446	Core poly

#### ALIGNMENTS

RESULT 1  
AAY89837  
ID AAY89837 standard; peptide; 36 AA.  
AC AAY89837;  
XX  
XX 23-MAY-2000 (first entry)  
XX  
XX Core polypeptide fragment T No. 1406.  
XX  
XX Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
XX HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
XX anti-fusogenic; differentiation factor; interleukin; interferon;  
XX colony stimulating factor; hormone; angiogenic factor.  
XX  
XX Unidentified.  
XX  
XX WO9595615-A1.  
XX  
XX 25-NOV-1999.  
XX  
XX 20-MAY-1999; 99WO-US011219.  
XX  
XX 20-MAY-1998; 98US-00082279.  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI; 2000-136792/12.  
XX  
XX A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX comprises enhancer sequence.  
XX  
XX Disclosure; Page 45; 124pp; English.  
XX  
XX The invention relates to hybrid polypeptides comprising enhancer peptide  
XX sequence linked to core polypeptides. The enhancer polypeptides are  
XX derived from various retroviral envelope (gp41) protein sequences,  
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
XX pharmacokinetic properties such as increasing the half-life of any core  
XX polypeptide that they are linked to. The core polypeptides are any  
XX polypeptide that may be introduced into a living system and that can  
XX function as a pharmacologically useful peptide for the treatment or  
XX prevention of a disease. The core polypeptides are bioactive peptides  
XX selected from a growth factor, cytokine, differentiation factor,  
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic



Query Match 100.0%; Score 36; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQOQKNEQELLELDKWASLWNWF 36  
 DB 1 YNTIYTLLEESQOQKNEQELLELDKWASLWNWF 36

RESULT 4  
 AAB78238  
 ID AAB78238 standard; peptide; 36 AA.  
 XX AAB78238;  
 DT 19-APR-2001 (first entry)  
 XX Core polypeptide T1406.  
 XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;  
 KW antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;  
 KW fusion-related disorder; bacterial infection; viral infection.  
 XX Unidentified.  
 OS  
 XX WO200103723-A1.  
 PN 18-JAN-2001.  
 XX 10-JUL-2000; 2000WO-US018772.  
 PF 09-JUL-1999; 99US-00350641.  
 PR (TRIM-) TRIMERIS INC.  
 PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI; 2001-147136/15.  
 DR  
 XX New hybrid polypeptide, useful for preventing, treating and diagnosing  
 PT e.g. viral infections, comprises an enhancer peptide linked to a core  
 PT polypeptide.  
 XX Disclosure; Page 58; 15lpp; English.  
 PS The present sequence is a core polypeptide which may be linked to an  
 XX enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of the  
 CC core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving coiled-  
 CC coil peptide interactions. Other uses include preventing, treating and/or  
 CC diagnosing disorders involving fusion events (e.g. modulation of  
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes  
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral  
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral  
 CC infections caused by human immunodeficiency virus, respiratory syncytial  
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and  
 CC polio virus). The enhancer peptide sequence increases the half-life and  
 CC reduces the clearance rate of therapeutic peptides, which increases their  
 CC efficacy and minimises the incidence and severity of adverse side  
 CC effects. In addition, this increases the sensitivity of the diagnostic  
 CC procedure in which they are used  
 XX SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQOQKNEQELLELDKWASLWNWF 36

DB 1 YNTIYTLLEESQOQKNEQELLELDKWASLWNWF 36

RESULT 5  
 AAB78237  
 ID AAB78237 standard; peptide; 36 AA.  
 XX AAB78237;  
 DT 19-APR-2001 (first entry)  
 XX Core polypeptide T1405.  
 DE Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;  
 XX antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;  
 KW fusion-related disorder; bacterial infection; viral infection.  
 XX Unidentified.  
 OS  
 XX WO200103723-A1.  
 PN 18-JAN-2001.  
 XX 10-JUL-2000; 2000WO-US018772.  
 PF 09-JUL-1999; 99US-00350641.  
 PR (TRIM-) TRIMERIS INC.  
 PA Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI; 2001-147136/15.  
 DR  
 XX New hybrid polypeptide, useful for preventing, treating and diagnosing  
 PT e.g. viral infections, comprises an enhancer peptide linked to a core  
 PT polypeptide.  
 XX Disclosure; Page 58; 15lpp; English.  
 PS The present sequence is a core polypeptide which may be linked to an  
 XX enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of the  
 CC core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving coiled-  
 CC coil peptide interactions. Other uses include preventing, treating and/or  
 CC diagnosing disorders involving fusion events (e.g. modulation of  
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes  
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral  
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral  
 CC infections caused by human immunodeficiency virus, respiratory syncytial  
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and  
 CC polio virus). The enhancer peptide sequence increases the half-life and  
 CC reduces the clearance rate of therapeutic peptides, which increases their  
 CC efficacy and minimises the incidence and severity of adverse side  
 CC effects. In addition, this increases the sensitivity of the diagnostic  
 CC procedure in which they are used  
 XX SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQOQKNEQELLELDKWASLWNWF 36  
 DB 1 YNTIYTLLEESQOQKNEQELLELDKWASLWNWF 36

RESULT 6  
 AAU70190

ID AAU70180 standard; peptide; 36 AA.  
 AC AAU70180;  
 XX  
 DT 14-FEB-2002 (first entry)  
 DE HIV viral envelope protein stabilising peptide #2.  
 DE Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;  
 KW anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;  
 KW alpha-helical region; ectodomain.  
 XX Homo sapiens.  
 OS  
 XX WO200170262-A2.  
 PN  
 XX 27-SEP-2001.  
 PD  
 XX 15-MAR-2001; 2001WO-US008108.  
 PF  
 XX 17-MAR-2000; 2000US-0189981P.  
 PR  
 XX (PANA-) PANACOS PHARM INC.  
 PA  
 XX Wild CT, Allaway GP;  
 PI  
 XX WPI; 2001-626098/72.  
 DR  
 XX Immunogenic composition for inhibiting HIV infection, comprises viral  
 PT envelope protein or its fragment exterior to viral membrane, a  
 PT stabilising peptide, and, optionally, viral cell surface receptor or its  
 PT fragment.  
 PT  
 XX Claim 6; Page 45; 84pp; English.  
 PS  
 XX The invention relates to methods of generating immunogens that elicit  
 CC neutralising antibodies which target regions of viral envelope proteins  
 CC such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-  
 CC 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and  
 CC AAU70677-AAU70743 represent stabilising peptides modelling the alpha-  
 CC helical regions of the ectodomain of the HIV-1 transmembrane protein to  
 CC stabilise fusion-active intermediate structures, which can be used as  
 CC vaccine immunogens. Immunogenic compositions comprise a viral envelope  
 CC protein or its fragment exterior to the viral membrane, a stabilising  
 CC peptide to disrupt formation of structural intermediates necessary for  
 CC viral fusion and entry, and optionally, a viral cell surface receptor or  
 CC its fragment. The stabilising peptide is capable of associating with the  
 CC envelope protein or its fragment to form a stabilised, fusion active  
 CC structure. Antibody binding assays are used to determine the ability of  
 CC immunogen vaccines to generate an immune response to various forms of  
 CC envelope. Virus neutralisation assays can be used to characterise the  
 CC antibody response raised against HIV-1 gp41 domains. The sequences and  
 CC methods are useful for inhibiting HIV infection, for inducing an immune  
 CC response in an animal and for raising antibodies  
 XX  
 SQ Sequence 36 AA;  
 Query Match 100.0%; Score 36; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YNTYITLLEESQNOQEKNEQELLELDKWASLWNWF 36  
 Db 1 YNTYITLLEESQNOQEKNEQELLELDKWASLWNWF 36  
 RESULT 7  
 ABB02830  
 ID ABB02830 standard; peptide; 36 AA.  
 XX  
 AC ABB02830;  
 XX  
 DT 11-SEP-2003 (revised)  
 DE Viral DP178/107-like region peptide T1406.  
 XX  
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 XX infection.  
 OS Viruses.  
 XX

DT 06-AUG-2003 (revised)  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Viral core polypeptide, SEQ ID NO: 1357.  
 XX  
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.  
 XX Viruses.  
 OS  
 XX WO200164013-A2.  
 PN  
 XX 07-SEP-2001.  
 PD  
 XX 07-FEB-2001; 2001WO-US003988.  
 PF  
 XX 29-FEB-2000; 2000US-00515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 PI WPI; 2001-514829/56.  
 XX  
 DR Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 XX fusion, useful for treating HIV and Respiratory Syncytial virus  
 PT infection.  
 PT  
 XX Disclosure; Page 524; 587pp; English.  
 PS  
 XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
 CC regions of proteins interact non-covalently with each other and/or with  
 CC peptides derived from them. This interaction is required for normal  
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
 CC peptide analogues may be used to inhibit respiratory syncytial virus  
 CC (RSV) infection in a cell. They may also be used to inhibit HIV  
 CC infection. The present sequence is a peptide provided in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
 CC 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 36 AA;  
 Query Match 100.0%; Score 36; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YNTYITLLEESQNOQEKNEQELLELDKWASLWNWF 36  
 Db 1 YNTYITLLEESQNOQEKNEQELLELDKWASLWNWF 36  
 RESULT 8  
 ABB01245  
 ID ABB01245 standard; peptide; 36 AA.  
 XX  
 AC ABB01245;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 06-AUG-2003 (revised)  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Viral DP178/107-like region peptide T1406.  
 XX  
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.  
 XX Viruses.  
 OS  
 XX

PN WO200164013-A2.  
 XX  
 PD 07-SEP-2001.  
 XX  
 XX 07-FEB-2001; 2001WO-US003988.  
 PF  
 XX 29-FEB-2000; 2000US-00515965.  
 XX  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 PI  
 XX WPI; 2001-514829/56.  
 DR  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection.  
 XX  
 XX Disclosure; Page 58; 587pp; English.  
 PS  
 XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DPI178 and DPI07. DPI178 and DPI07 correspond to amino acids 638-  
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
 CC regions of proteins interact non-covalently with each other and/or with  
 CC peptides derived from them. This interaction is required for normal  
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
 CC (RSV) infection in a cell. They may also be used to inhibit HIV  
 CC infection. The present sequence is a peptide provided in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
 CC 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 36 AA;  
  
 Query Match 100.0%; Score 36; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 YNTNTYTLLEESQNOQKEQELLELDKWASLWNWF 36  
 Db 1 YNTNTYTLLEESQNOQKEQELLELDKWASLWNWF 36  
  
 RESULT 9  
 ABB01244  
 ID ABB01244 standard; peptide; 36 AA.  
 XX  
 AC ABB01244;  
 XX  
 XX 11-SEP-2003 (revised)  
 DT 06-AUG-2003 (revised)  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Viral DPI178/107-like region peptide T1405.  
 XX  
 XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.  
 KW  
 XX Viruses.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note= "N-terminal is substituted by Ac"  
 FT Modified-site 36  
 FT /note= "C-terminal amide"  
 XX  
 XX WO200164013-A2.  
 PN  
 XX 07-SEP-2001.  
 PD  
 XX 07-FEB-2001; 2001WO-US003988.  
 PF

XX 29-FEB-2000; 2000US-00515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 PI  
 XX WPI; 2001-514829/56.  
 DR  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection.  
 XX  
 XX Disclosure; Page 58; 587pp; English.  
 PS  
 XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DPI178 and DPI07. DPI178 and DPI07 correspond to amino acids 638-  
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
 CC regions of proteins interact non-covalently with each other and/or with  
 CC peptides derived from them. This interaction is required for normal  
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
 CC (RSV) infection in a cell. They may also be used to inhibit HIV  
 CC infection. The present sequence is a peptide provided in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
 CC 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 36 AA;  
  
 Query Match 100.0%; Score 36; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 YNTNTYTLLEESQNOQKEQELLELDKWASLWNWF 36  
 Db 1 YNTNTYTLLEESQNOQKEQELLELDKWASLWNWF 36  
  
 RESULT 10  
 AAU13791  
 ID AAU13791 standard; peptide; 36 AA.  
 XX  
 AC AAU13791;  
 XX  
 XX 21-NOV-2001 (first entry)  
 DT  
 DE DPI178-like/DPI07-like peptide T-1406.  
 XX  
 XX Anti-retroviral; DPI178-like; DPI07-like; transmembrane protein gp41;  
 KW antifusogenic; antiviral; HIV transmission; mutant; mutein.  
 KW  
 XX Human immunodeficiency virus 1; isolate LAI.  
 OS Synthetic.  
 OS  
 XX WO200151673-A2.  
 PN  
 XX 19-JUL-2001.  
 PD  
 XX 05-JUL-2000; 2000WO-US035727.  
 PF  
 XX 09-JUL-1999; 99US-00350841.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
 PI  
 XX WPI; 2001-442157/47.  
 DR  
 XX Identifying a compound that inhibits the formation of or disrupts a  
 PT DPI07/DPI178 complex, especially compounds with antifusogenic, antiviral  
 PT or intracellular modulatory activity, by detecting the formation of a  
 PT DPI07/DPI178 complex.

XX PS Disclosure; Page 77; 259pp; English.

XX CC The present invention relates to peptides which exhibit anti-retroviral

CC activity. The peptides of the invention (AAU12559-AAU14009) comprise

CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to

CC amino acids 639-673 of the transmembrane protein gp41 from human

CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide

CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention

CC also relates to a method of identifying compounds that inhibit the

CC formation of or disrupts a DP107/DP178 complex. The method comprises

CC detecting the formation of a DP107/DP178 complex, both in the presence or

CC absence of a test compound, in a reaction mixture containing DP107 and

CC DP178 peptides. The method is useful for identifying compounds, including

CC small molecule compounds, which may themselves exhibit antifusogenic,

CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like

CC peptides are useful to inhibit human and non-human retroviral,

CC particularly HIV, transmission to uninfected cells. The present sequence

CC represents one of the DP178-like/DP107-like peptides of the invention

XX SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;

Best Local Similarity 100.0%; Pred. No. 3.3e-27;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNTIYTLLESQNOQEKNEQELLELDKWASLWNWF 36

Db 1 YNTNTIYTLLESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 11

AAU13790

ID AAU13790 standard; peptide; 36 AA.

XX AC AAU13790;

XX DT 21-NOV-2001 (first entry)

XX DE DP178-like/DP107-like peptide T-1405.

XX KW Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;

XX KW antifusogenic; antiviral; HIV transmission; mutant; mutein.

XX OS Human immunodeficiency virus 1; isolate LAI.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal is substituted by Ac"

FT Modified-site 36

FT /note= "C-terminal amide"

PN WO200151673-A2.

XX PN 19-JUL-2001.

XX PD 05-JUL-2000; 2000WO-US035727.

XX PP 09-JUL-1999; 99US-00350841.

XX PR (TRIM-) TRIMERIS INC.

XX PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;

XX DR WPI; 2001-442157/47.

XX PT Identifying a compound that inhibits the formation of or disrupts a

PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral

PT or intracellular modulatory activity, by detecting the formation of a

PT DP107/DP178 complex.

XX PS Disclosure; Page 77; 259pp; English.

XX CC The present invention relates to peptides which exhibit anti-retroviral

CC activity. The peptides of the invention (AAU12559-AAU14009) comprise

CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to

CC amino acids 639-673 of the transmembrane protein gp41 from human

CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide

CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention

CC also relates to a method of identifying compounds that inhibit the

CC formation of or disrupts a DP107/DP178 complex. The method comprises

CC detecting the formation of a DP107/DP178 complex, both in the presence or

CC absence of a test compound, in a reaction mixture containing DP107 and

CC DP178 peptides. The method is useful for identifying compounds, including

CC small molecule compounds, which may themselves exhibit antifusogenic,

CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like

CC peptides are useful to inhibit human and non-human retroviral,

CC particularly HIV, transmission to uninfected cells. The present sequence

CC represents one of the DP178-like/DP107-like peptides of the invention

XX SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;

Best Local Similarity 100.0%; Pred. No. 3.3e-27;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNTIYTLLESQNOQEKNEQELLELDKWASLWNWF 36

Db 1 YNTNTIYTLLESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 12

AAO18772

ID AAO18772 standard; peptide; 36 AA.

XX AC AAO18772;

XX DT 29-OCT-2002 (first entry)

XX DE HIV gp41 protein DP-178 region derived peptide SEQ ID NO: 3.

XX KW Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;

XX KW gp41.

XX OS Human immunodeficiency virus.

XX PN WO200256902-A2.

XX PD 25-JUL-2002.

XX PF 17-DEC-2001; 2001WO-US048802.

XX PR 19-DEC-2000; 2000US-0256657P.

XX PA (SCHE ) SCHERING CORP.

XX PI Baroudy BM;

XX DR WPI; 2002-636513/68.

XX PT Treatment of HIV infection in an individual involves administration of a

PT combination of chemokine co-receptor five antagonist and a specified HIV

PT envelope polypeptide.

XX PS Disclosure; Page 32; 52pp; English.

XX CC The present invention relates to a method of treating an HIV infection in

CC an individual, which involves administering in combination a chemokine co

CC -receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its

CC derivative. Other viral infections can also be treated using the method.

CC The present sequence is a peptide derived from HIV and useful in the

CC method of the invention

XX SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESQKQKNEQELLELDKWASLWNWF 36  
|||||  
Db 1 YNTYITLLEESQKQKNEQELLELDKWASLWNWF 36  
|||||

RESULT 13  
ADE02850  
ID ADE02850 standard; peptide; 36 AA.  
XX  
AC ADE02850;  
XX  
XX 29-JAN-2004 (first entry)  
DT  
DE Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1357.  
XX  
XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;  
KW pharmacokinetic; fusogenic; insulin; diabetes.  
XX  
OS Unidentified.  
XX  
PN US6348568-B1.  
XX  
PD 19-FEB-2002.  
XX  
PF 20-MAY-1999; 99US-00315304.  
XX  
PR 20-MAY-1998; 98US-00082279.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
DR WPI; 2002-424396/45.

XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral  
PT activity, has enhancer peptide sequence derived from retroviral envelope  
PT protein sequences linked to core polypeptide e.g. therapeutic protein.  
XX  
PS Disclosure; SEQ ID NO 1357; 70pp; English.

XX The invention relates to a novel hybrid polypeptide comprising an  
CC enhancer peptide sequence linked to a core polypeptide. The enhancer  
CC peptide sequence comprises QWEQKI or WASLWEP. The invention also  
CC includes novel peptides that exhibit anti-fusogenic activity, antiviral  
CC activity and/or ability to modulate intracellular processes. The novel  
CC hybrid polypeptide has virucide and antidiabetic activity. The enhancer  
CC peptide sequence enhances pharmacokinetic properties of any core  
CC polypeptide, for example, a polypeptide useful for the treatment or  
CC prevention of a disease, or an imaging agent useful for imaging  
CC structures in vivo. The core polypeptides and hybrid polypeptides are  
CC useful for modulating fusogenic events and exhibit antifusogenic or  
CC antiviral activity. The novel hybrid polypeptide is useful for decreasing  
CC viral infection and modulating intracellular processes involving coiled-  
CC coil peptide interactions. The novel hybrid polypeptide comprises insulin  
CC or its fragment, so the core polypeptide is useful for ameliorating the  
CC symptoms of forms of diabetes. The novel hybrid polypeptide is also  
CC useful as a part of prognosis for preventing disorders including fusion  
CC events and viral infection that involves cell-cell and/or virus-cell  
CC fusion, and for diagnosis and in vivo imaging methods. This sequence  
CC represents an enhancer peptide of the invention.

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESQKQKNEQELLELDKWASLWNWF 36  
|||||

Db 1 YNTYITLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 14

ADE02716  
ID ADE02716 standard; peptide; 36 AA.  
XX  
AC ADE02716;  
XX

XX 29-JAN-2004 (first entry)  
DT  
DE Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1223.  
XX  
XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;  
KW pharmacokinetic; fusogenic; insulin; diabetes.  
XX  
OS Unidentified.

XX Key Location/Qualifiers  
PH Modified-site 1  
FT Modified-site 36 /note= "Residue is modified by acetyl group"  
FT Modified-site 36 /note= "C-terminal amide"  
XX

PN US6348568-B1.

XX 19-FEB-2002.

XX 20-MAY-1999; 99US-00315304.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2002-424396/45.

XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral  
PT activity, has enhancer peptide sequence derived from retroviral envelope  
PT protein sequences linked to core polypeptide e.g. therapeutic protein.

XX Disclosure; SEQ ID NO 1223; 70pp; English.

XX The invention relates to a novel hybrid polypeptide comprising an  
CC enhancer peptide sequence linked to a core polypeptide. The enhancer  
CC peptide sequence comprises QWEQKI or WASLWEP. The invention also  
CC includes novel peptides that exhibit anti-fusogenic activity, antiviral  
CC activity and/or ability to modulate intracellular processes. The novel  
CC hybrid polypeptide has virucide and antidiabetic activity. The enhancer  
CC peptide sequence enhances pharmacokinetic properties of any core  
CC polypeptide, for example, a polypeptide useful for the treatment or  
CC prevention of a disease, or an imaging agent useful for imaging  
CC structures in vivo. The core polypeptides and hybrid polypeptides are  
CC useful for modulating fusogenic events and exhibit antifusogenic or  
CC antiviral activity. The novel hybrid polypeptide is useful for decreasing  
CC viral infection and modulating intracellular processes involving coiled-  
CC coil peptide interactions. The novel hybrid polypeptide comprises insulin  
CC or its fragment, so the core polypeptide is useful for ameliorating the  
CC symptoms of forms of diabetes. The novel hybrid polypeptide is also  
CC useful as a part of prognosis for preventing disorders including fusion  
CC events and viral infection that involves cell-cell and/or virus-cell  
CC fusion, and for diagnosis and in vivo imaging methods. This sequence  
CC represents an enhancer peptide of the invention.

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESQKQKNEQELLELDKWASLWNWF 36  
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Search completed: March 6, 2006, 16:19:04  
Job time : 118.333 secs

Db 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36

## RESULT 15

ABO10164  
ID ABO10164 standard; peptide; 36 AA.

XX AC ABO10164;  
XX 23-OCT-2003 (revised)  
DT 19-AUG-2003 (first entry)  
XX  
XX HIV1-SF2 gp41 protein, DP85 peptide.  
XX  
XX HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;  
KW Epstein-Barr virus infection; heptad repeat motif.  
XX  
XX Human immunodeficiency virus 1; isolate SF2.

XX US6518013-B1.

XX 11-FEB-2003.

XX 07-JUN-1995; 95US-00485546.

XX 07-JUN-1993; 93US-00073028.

PR 07-JUN-1994; 94US-00255208.

PR 20-DEC-1994; 94US-00360107.

XX (TRIM-) TRIMERIS INC.

PA Barney SO, Lambert DM, Petteway SR;

XX WPI; 2003-465599/44.

XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting  
PT the cell with a peptide consisting of a region of Epstein-Barr virus  
PT protein.

XX Example; Fig 1; 716pp; English.

XX The invention relates to inhibiting (M) transmission of an Epstein-Barr  
CC virus to a cell, comprising contacting the cell with an effective  
CC concentration of a peptide consisting of a region of 16-39 consecutive  
CC amino acids of an Epstein-Barr virus protein for an effective period of  
CC time, where the region is recognised by one or more of ALLM015,  
CC 107X178x4 or PLZIP sequence search motifs, the peptide further comprises  
CC an amino terminal X, and a carboxy terminal Z in which X comprises an  
CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic  
CC group or macromolecular carrier group, and Z comprises a carboxyl group,  
CC amide group, hydrophobic group, or macromolecular carrier group, and  
CC fusion of the virus to the cell is inhibited. The peptides were  
CC identified by analysing the structure/motifs present in the HIV-1  
CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat  
CC motif containing peptides were used to design the motifs cited above,  
CC which in turn were used to analyse proteins from other pathogenic  
CC organisms and HIV isolates, looking for DP107/178 structural analogues.  
CC The method is useful for inhibiting transmission of Epstein-Barr virus to  
CC a cell and Epstein-Barr virus infection. The present sequence is a  
CC control peptide used in the study of the DP178 structure. (Updated on 23-  
CC OCT-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 6; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.3e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36

DB 1 YNTYITLLSESONQOEKNEQELLELDKWASLWNWF 36



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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:50:56 ; Search time 10 Seconds  
(without alignments)  
72.002 Million cell updates/sec

Title: US-09-809-060A-2

Perfect score: 198

Sequence: 1 YNTYITLLEESQNOEKNEQELLELDKQASLWVNF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 78453

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New.\*

- 1: /cgn2\_6/prodata/2/pubpa/US08\_NEW\_PUB.pap.\*
- 2: /cgn2\_6/prodata/2/pubpa/US06\_NEW\_PUB.pap.\*
- 3: /cgn2\_6/prodata/2/pubpa/US07\_NEW\_PUB.pap.\*
- 4: /cgn2\_6/prodata/2/pubpa/PCT\_NEW\_PUB.pap.\*
- 5: /cgn2\_6/prodata/2/pubpa/US09\_NEW\_PUB.pap.\*
- 6: /cgn2\_6/prodata/2/pubpa/US10\_NEW\_PUB.pap.\*
- 7: /cgn2\_6/prodata/2/pubpa/US11\_NEW\_PUB.pap.\*
- 8: /cgn2\_6/prodata/2/pubpa/US60\_NEW\_PUB.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	176	88.9	36	US-10-841-956A-1	Sequence 1, Appli
2	176	88.9	36	US-11-029-003-1	Sequence 1, Appli
3	176	88.9	36	US-11-187-687-22	Sequence 22, Appli
4	176	88.9	37	US-11-112-277-33	Sequence 33, Appli
5	176	88.9	44	US-11-187-687-24	Sequence 24, Appli
6	164	82.8	44	US-11-089-426-10	Sequence 10, Appli
7	138	69.7	36	US-10-506-796A-7	Sequence 7, Appli
8	137	69.2	36	US-10-506-796A-5	Sequence 5, Appli
9	135	68.2	35	US-10-506-796A-1	Sequence 1, Appli
10	135	68.2	36	US-10-506-796A-3	Sequence 3, Appli
11	133	67.2	36	US-10-506-796A-6	Sequence 6, Appli
12	124	62.6	39	US-10-841-956A-3	Sequence 3, Appli
13	124	62.6	39	US-11-029-003-3	Sequence 3, Appli
14	124	62.6	40	US-11-112-277-34	Sequence 34, Appli
15	123	62.1	36	US-10-506-796A-4	Sequence 4, Appli
16	104	52.5	38	US-11-151-598-4	Sequence 4, Appli
17	99	50.0	34	US-11-112-277-6	Sequence 6, Appli
18	99	50.0	34	US-11-112-277-38	Sequence 38, Appli
19	99	50.0	34	US-11-151-598-10	Sequence 10, Appli
20	99	50.0	34	US-11-151-598-12	Sequence 12, Appli
21	99	50.0	35	US-11-112-277-7	Sequence 7, Appli
22	99	50.0	35	US-11-112-277-37	Sequence 37, Appli
23	99	50.0	47	US-11-151-598-5	Sequence 5, Appli
24	97	49.0	34	US-11-112-277-8	Sequence 8, Appli
25	97	49.0	34	US-11-112-277-36	Sequence 36, Appli

26 89 44.9 15 7 US-11-045-024-13381. Sequence 13381, A  
27 80 40.4 15 7 US-11-045-024-13388. Sequence 13388, A  
28 79 39.9 15 7 US-11-045-024-12922. Sequence 12922, A  
29 73 36.9 15 7 US-11-045-024-13379. Sequence 13379, A  
30 72 36.4 11 7 US-11-045-024-8659. Sequence 8659, Ap  
31 71 35.9 11 7 US-11-045-024-103. Sequence 103, App  
32 71 35.9 11 7 US-11-045-024-3968. Sequence 3968, Ap  
33 71 35.9 11 7 US-11-045-024-7039. Sequence 7039, Ap  
34 68 34.3 10 7 US-11-045-024-5568. Sequence 5568, Ap  
35 66 33.3 11 7 US-11-045-024-102. Sequence 102, App  
36 66 33.3 11 7 US-11-045-024-3967. Sequence 3967, Ap  
37 66 33.3 11 7 US-11-045-024-6943. Sequence 6943, Ap  
38 64 32.3 35 7 US-11-112-277-40. Sequence 40, Appl  
39 64 32.3 36 7 US-11-112-277-39. Sequence 39, Appl  
40 62 31.3 9 7 US-11-045-024-3776. Sequence 3776, Ap  
41 62 31.3 9 7 US-11-045-024-5533. Sequence 5533, Ap  
42 62 31.3 9 7 US-11-045-024-12581. Sequence 12581, A  
43 62 31.3 11 7 US-11-045-024-101. Sequence 101, App  
44 62 31.3 11 7 US-11-045-024-3966. Sequence 3966, Ap  
45 62 31.3 11 7 US-11-045-024-3969. Sequence 3969, Ap

#### ALIGNMENTS

RESULT 1  
US-10-841-956A-1  
; Sequence 1, Application US/10841956A  
; Publication No. US20050281829A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN HEHIR, CRISTINA A.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: STATTEL, JAMES M.  
; APPLICANT: PALOMBELLA, VITO J.  
; APPLICANT: BITONTI, ALAN R.  
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS  
; FILE REFERENCE: 08945.0003-00000  
; CURRENT APPLICATION NUMBER: US/10/841,956A  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: 60/468,835  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-841-956A-1

Query Match 88.9%; Score 176; DB 6; Length 36;  
Best Local Similarity 86.1%; Pred. No. 1.7e-15;  
Matches 31; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
QY 1 YNTYITLLEESQNOEKNEQELLELDKQASLWVNF 36  
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Db 1 YTSLSHLSLEESQNOEKNEQELLELDKQASLWVNF 36

RESULT 2  
US-11-029-003-1  
; Sequence 1, Application US/11029003  
; Publication No. US20050260194A1  
; GENERAL INFORMATION:  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: RIVERA, DANIEL S.  
; APPLICANT: BITONTI, ALAN J.  
; APPLICANT: STATTEL, JAMES  
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS  
; FILE REFERENCE: 08945.0007-01000  
; CURRENT APPLICATION NUMBER: US/11/029,003  
; CURRENT FILING DATE: 2005-01-05



```

; APPLICANT: Wesolowski, John
; TITLE OF INVENTION: Fc Fusion Proteins For Enhancing the Immunogenicity of
; TITLE OF INVENTION: Protein and Peptide Antigens
; FILE REFERENCE: LEX-007
; CURRENT APPLICATION NUMBER: US/11/089,426
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US/09/621,268
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/144,965
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fused
; OTHER INFORMATION: polypeptide from pDC-muFC vector
US-11-089-426-10

Query Match      82.8%; Score 164; DB 7; Length 44;
Best Local Similarity 90.6%; Pred. No. 6e-14;
Matches 29; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTLLESQSQKNEQELLELDKQWASLWNP 36
   |||||:|||||:|||||:|||||:|||||
DB 3 IHSLLSQSQKNEQELLELDKQWASLWNP 34
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RESULT 7
US-10-506-796A-7
; Sequence 7, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.000602
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: HIV-1 isolate 1924v3.20 (residues 649-685)
US-10-506-796A-7

Query Match      69.7%; Score 138; DB 6; Length 36;
Best Local Similarity 96.0%; Pred. No. 7.3e-11;
Matches 24; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 SQNQEKNEQELLELDKQWASLWNP 36
   |||||:|||||:|||||:|||||:|||||
DB 1 SQNQEKNEQELLELDKQWASLWNP 25
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RESULT 8
US-10-506-796A-5
; Sequence 5, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.000602
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(35)
; OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
US-10-506-796A-5

Query Match      68.2%; Score 135; DB 6; Length 35;
Best Local Similarity 96.0%; Pred. No. 1.7e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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   |||||:|||||:|||||:|||||:|||||
DB 1 SQTQEKNEQELLELDKQWASLWNP 25
   |||||:|||||:|||||:|||||:|||||

RESULT 9
US-10-506-796A-1
; Sequence 1, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.000602
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(35)
; OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
US-10-506-796A-1

Query Match      69.2%; Score 137; DB 6; Length 36;
Best Local Similarity 96.0%; Pred. No. 9.7e-11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SQNQEKNEQELLELDKQWASLWNP 36
   |||||:|||||:|||||:|||||:|||||
DB 1 SQNQEKNEQELLELDKQWASLWNP 25
   |||||:|||||:|||||:|||||:|||||
```

```

; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.000602
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: HIV-1 isolate 593 clone (residues 649-685)
US-10-506-796A-5

Query Match      69.2%; Score 137; DB 6; Length 36;
Best Local Similarity 96.0%; Pred. No. 9.7e-11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SQNQEKNEQELLELDKQWASLWNP 36
   |||||:|||||:|||||:|||||:|||||
DB 1 SQNQEKNEQELLELDKQWASLWNP 25
   |||||:|||||:|||||:|||||:|||||

RESULT 9
US-10-506-796A-1
; Sequence 1, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.000602
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(35)
; OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
US-10-506-796A-1

Query Match      68.2%; Score 135; DB 6; Length 35;
Best Local Similarity 96.0%; Pred. No. 1.7e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SQNQEKNEQELLELDKQWASLWNP 36
   |||||:|||||:|||||:|||||:|||||
DB 1 SQTQEKNEQELLELDKQWASLWNP 25
   |||||:|||||:|||||:|||||:|||||

RESULT 10
US-10-506-796A-3
; Sequence 3, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
```

```
; APPLICANT: MOR, Tsafirir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.000602
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-506-796A-3

Query Match      68.2%; Score 135; DB 6; Length 36;
Best Local Similarity 96.0%; Pred. No. 1.7e-10;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 SQNQEKNEQELLELDKQASLWNWF 36
Db 2 SQNQEKNEQELLELDKQASLWNWF 26

RESULT 11
US-10-506-796A-6
; Sequence 6, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafirir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.000602
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: HIV-1 isolate 98BRRS012 (residues 649-685)
US-10-506-796A-6

Query Match      67.2%; Score 133; DB 6; Length 36;
Best Local Similarity 92.0%; Pred. No. 3e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 SQNQEKNEQELLELDKQASLWNWF 36
Db 1 SQNQEKNEHLELDKQANLWNWF 25

RESULT 12
US-10-841-956A-3
; Sequence 3, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-3

Query Match      62.6%; Score 124; DB 6; Length 39;
Best Local Similarity 71.9%; Pred. No. 4.1e-09;
Matches 23; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 IYTLLESQNOQEKNEQELLELDKQASLWNWF 36
Db 8 ITALLEQAQIQQEKNEYELQKLDKQASLWNWF 39

RESULT 13
US-11-029-003-3
; Sequence 3, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEL, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
; CURRENT APPLICATION NUMBER: US/11/029,003
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539,207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487,964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469,600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-029-003-3

Query Match      62.6%; Score 124; DB 7; Length 39;
Best Local Similarity 71.9%; Pred. No. 4.1e-09;
Matches 23; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 IYTLLESQNOQEKNEQELLELDKQASLWNWF 36
Db 8 ITALLEQAQIQQEKNEYELQKLDKQASLWNWF 39

RESULT 14
US-11-112-277-34
; Sequence 34, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-3
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FILE REFERENCE: 500862003700  
CURRENT APPLICATION NUMBER: US/11/112,277  
CURRENT FILING DATE: 2005-04-22  
PRIOR APPLICATION NUMBER: US 60/565,228  
PRIOR FILING DATE: 2004-04-23  
NUMBER OF SEQ ID NOS: 53  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 34  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: T1249 Analogue  
NAME/KEY: MOD\_RES  
LOCATION: 40  
OTHER INFORMATION: Xaa is Lys linked to ABEE-MPA  
US-11-112-277-34

Query Match 62.6%; Score 124; DB 7; Length 40;  
Best Local Similarity 71.9%; Pred. No. 4.2e-09;  
Matches 23; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 IYTLLEEQKNEQELLELDKWSLWVWF 36  
DB 8 ITALLEEQKNEQELLELDKWSLWVWF 39

RESULT 15  
US-10-506-796A-4  
Sequence 4, Application US/10506796A  
Publication No. US20060013831A1  
GENERAL INFORMATION:  
APPLICANT: MOR, Tsafir  
APPLICANT: MATOBA, Nobuyuki  
APPLICANT: ARNTZEN, Charles  
TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE  
FILE REFERENCE: 01231.000602  
CURRENT APPLICATION NUMBER: US/10/506,796A  
CURRENT FILING DATE: 2004-09-03  
PRIOR APPLICATION NUMBER: PCT/US03/07073  
PRIOR FILING DATE: 2003-03-06  
PRIOR APPLICATION NUMBER: 60/362,247  
PRIOR FILING DATE: 2002-03-06  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 4  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(35)  
OTHER INFORMATION: HIV-1 isolate MN clone v5 (residues 649-685)  
US-10-506-796A-4

Query Match 62.1%; Score 123; DB 6; Length 36;  
Best Local Similarity 88.0%; Pred. No. 5e-09;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 SQNQKNEQELLELDKWSLWVWF 36  
DB 1 SQTQKNEQELLELDKWSLWVWF 25

Search completed: March 6, 2006, 15:54:21  
Job time : 11 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 15:44:30 ; Search time 94 Seconds  
(without alignments)  
160.020 Million cell updates/sec

Title: US-09-809-060A-2  
Perfect score: 198  
Sequence: 1 YNTYITLLEESQNOQKNEQELLELDKWASLWNWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 549595

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:\*

- 1: /cgn2\_6/prodata1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/prodata1/pubpaa/US08\_PUBCOMB.pep:\*
- 3: /cgn2\_6/prodata1/pubpaa/US09\_PUBCOMB.pep:\*
- 4: /cgn2\_6/prodata1/pubpaa/US10A\_PUBCOMB.pep:\*
- 5: /cgn2\_6/prodata1/pubpaa/US10B\_PUBCOMB.pep:\*
- 6: /cgn2\_6/prodata1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	36	3	US-09-809-060-2
2	198	100.0	36	4	US-10-252-136-3
3	198	100.0	36	4	US-10-351-641-1357
4	198	100.0	36	4	US-10-267-682-3
5	198	100.0	36	4	US-10-267-748-3
6	198	100.0	36	4	US-10-663-589-38
7	198	100.0	36	4	US-10-671-282-38
8	198	100.0	36	5	US-10-168-295-3
9	198	100.0	36	5	US-10-950-010-3
10	198	100.0	36	6	US-11-066-697-1421
11	187	94.4	36	4	US-10-351-641-1051
12	185	93.4	36	3	US-09-809-060-22
13	185	93.4	36	3	US-09-779-451-47
14	185	93.4	36	4	US-10-351-641-856
15	185	93.4	36	4	US-10-685-801-47
16	185	93.4	36	4	US-10-660-206-47
17	185	93.4	46	3	US-09-809-060-20
18	185	93.4	46	3	US-09-779-451-45
19	185	93.4	46	4	US-10-685-801-45
20	185	93.4	46	4	US-10-660-206-45
21	183	92.4	46	3	US-09-854-816-109
22	181	91.4	36	4	US-10-351-641-642
23	181	91.4	36	4	US-10-457-780-52
24	181	91.4	36	5	US-10-950-010-535
25	181	91.4	36	5	US-10-950-010-537
26	180	90.9	36	5	US-10-950-010-540
27	178	89.9	36	3	US-09-809-060-3

28	178	89.9	36	4	US-10-252-136-4	Sequence 4, Appli
29	178	89.9	36	4	US-10-351-641-1358	Sequence 1358, Ap
30	178	89.9	36	4	US-10-351-641-1359	Sequence 1359, Ap
31	178	89.9	36	4	US-10-267-682-4	Sequence 4, Appli
32	178	89.9	36	4	US-10-267-748-4	Sequence 4, Appli
33	178	89.9	36	4	US-10-663-589-39	Sequence 39, Appl
34	178	89.9	36	4	US-10-671-282-39	Sequence 39, Appl
35	178	89.9	36	5	US-10-168-295-4	Sequence 4, Appli
36	178	89.9	36	5	US-10-950-010-4	Sequence 4, Appli
37	178	89.9	36	5	US-10-950-010-541	Sequence 541, App
38	178	89.9	36	6	US-11-066-697-1422	Sequence 1422, Ap
39	177	89.4	36	4	US-10-351-641-1515	Sequence 1515, Ap
40	176	88.9	36	3	US-09-809-060-1	Sequence 1, Appli
41	176	88.9	36	3	US-09-809-060-85	Sequence 85, Appl
42	176	88.9	36	3	US-09-796-202-10	Sequence 10, Appl
43	176	88.9	36	3	US-09-960-717-2	Sequence 2, Appli
44	176	88.9	36	3	US-09-779-451-5	Sequence 5, Appli
45	176	88.9	36	3	US-09-834-628-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-09-809-060-2  
; Sequence 2, Application US/09809060  
; Publication NO. US20020010317A1  
; GENERAL INFORMATION:  
; APPLICANT: Willd, Carl T.  
; APPLICANT: Allaway, Graham P.  
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit  
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active  
; FILE OF INVENTION: Regions of HIV Envelope Proteins  
; FILE REFERENCE: 1900.0260001  
; CURRENT APPLICATION NUMBER: US/09/809,060  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: US 60/189,981  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-809-060-2

Query Match 100.0%; Score 198; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.6e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YNTYITLLEESQNOQKNEQELLELDKWASLWNWF 36  
DB 1 YNTYITLLEESQNOQKNEQELLELDKWASLWNWF 36

RESULT 2  
US-10-252-136-3  
; Sequence 3, Application US/10252136  
; Publication NO. US20030103998A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, M. Ross  
; APPLICANT: Lambert, Dennis M.  
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER  
; TITLE OF INVENTION: VIRAL INFECTIONS  
; TITLE OF INVENTION: USING COMBINATORY THERAPY  
; FILE REFERENCE: 7872-036  
; CURRENT APPLICATION NUMBER: US/10/252,136  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: US/08/973,952  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3

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; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-3

Query Match          100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 3
US-10-351-641-1357
; Sequence 1357, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M. D.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1357
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1357

Query Match          100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 4
US-10-267-682-3
; Sequence 3, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 5
US-10-267-748-3
; Sequence 3, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-267-682-3

Query Match          100.0%; Score 198; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 5
US-10-267-748-3
; Sequence 3, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
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10  
FILING DATE: 08-Oct-2002  
CLASSIFICATION: <Unknown>  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/484,223A  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-267-748-3

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.6e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQEKNEQELLELDKWSLWNNWF 36  
DB 1 YNTIYTLLEESQNOQEKNEQELLELDKWSLWNNWF 36

RESULT 6  
US-10-663-589-38  
Sequence 38, Application US/10663589  
Publication No. US20040063637A1  
GENERAL INFORMATION:  
APPLICANT: Trimeris, Inc.  
TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV  
TITLE OF INVENTION: gp41-derived peptides, and its use in therapy  
FILE REFERENCE: TRM-003  
CURRENT APPLICATION NUMBER: US/10/663,589  
CURRENT FILING DATE: 2003-09-16  
PRIOR APPLICATION NUMBER: US 60/414,441  
PRIOR FILING DATE: 2002-09-27  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 38  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: synthesized  
US-10-663-589-38

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.6e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQEKNEQELLELDKWSLWNNWF 36  
DB 1 YNTIYTLLEESQNOQEKNEQELLELDKWSLWNNWF 36

RESULT 7  
US-10-671-282-38  
Sequence 38, Application US/10671282  
Publication No. US20040122214A1  
GENERAL INFORMATION:  
APPLICANT: Trimeris, Inc.  
TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and  
TITLE OF INVENTION: their use in therapy  
FILE REFERENCE: TRM-004

10  
CURRENT APPLICATION NUMBER: US/10/671,282  
CURRENT FILING DATE: 2003-09-24  
PRIOR APPLICATION NUMBER: 60/414,439  
PRIOR FILING DATE: 2002-09-27  
NUMBER OF SEQ ID NOS: 114  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 38  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: synthesized  
US-10-671-282-38

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.6e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQEKNEQELLELDKWSLWNNWF 36  
DB 1 YNTIYTLLEESQNOQEKNEQELLELDKWSLWNNWF 36

RESULT 8  
US-10-168-295-3  
Sequence 3, Application US/10168295  
Publication No. US20050065319A1  
GENERAL INFORMATION:  
APPLICANT: Baroudy, Bahige M.  
TITLE OF INVENTION: Combination Method For Treating Viral Infections  
FILE REFERENCE: IN01358  
CURRENT APPLICATION NUMBER: US/10/168,295  
CURRENT FILING DATE: 2002-06-19  
PRIOR APPLICATION NUMBER: PCT/US01/48802  
PRIOR FILING DATE: 2000-12-17  
PRIOR APPLICATION NUMBER: 60/256,657  
PRIOR FILING DATE: 2000-12-19  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 3  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Human immunodeficiency virus type 1  
US-10-168-295-3

Query Match 100.0%; Score 198; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 6.6e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQEKNEQELLELDKWSLWNNWF 36  
DB 1 YNTIYTLLEESQNOQEKNEQELLELDKWSLWNNWF 36

RESULT 9  
US-10-950-010-3  
Sequence 3, Application US/10950010  
Publication No. US20050070475A1  
GENERAL INFORMATION:  
APPLICANT: BRIDON, Dominique P.  
APPLICANT: DUFRESNE, Robert S.  
APPLICANT: BOUDJELILAB, Nissab  
APPLICANT: ROBITAILLE, Martin  
APPLICANT: MILNER, Peter G.  
TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL  
TITLE OF INVENTION: INFECTION  
FILE REFERENCE: 500862001501/REDC-1512  
CURRENT APPLICATION NUMBER: US/10/950,010  
CURRENT FILING DATE: 2004-09-24  
PRIOR APPLICATION NUMBER: US 09/623,533  
PRIOR FILING DATE: 2000-09-05  
PRIOR APPLICATION NUMBER: PCT/US00/13651  
PRIOR FILING DATE: 2000-05-17



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; FILE REFERENCE: 1900.0300003
; CURRENT APPLICATION NUMBER: US/09/779,451
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/235,901
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/181,543
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-779-451-47

Query Match          93.4%; Score 185; DB 3; Length 36;
Best Local Similarity 91.7%; Pred. No. 2.2e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWSLWNWF 36
   |||:|||||:|||||:|||||:|||||:|||||
Db 1 YTSEIYTLLEESNQOEKNEQELLELDKWSLWNWF 36

RESULT 14
US-10-351-641-856
; Sequence 856, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 856
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-856

Query Match          93.4%; Score 185; DB 4; Length 36;
Best Local Similarity 94.4%; Pred. No. 2.2e-14;
Matches 34; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWSLWNWF 36
   |||:|||||:|||||:|||||:|||||:|||||
Db 1 YTKFIYTLLEESNQOEKNEQELLELDKWSLWNWF 36

RESULT 15
US-10-685-801-47
; Sequence 47, Application US/10685801
; Publication No. US20040132011A1
; GENERAL INFORMATION:
; APPLICANT: Allaway, Graham P.
; APPLICANT: Wild, Carl T.
; APPLICANT: Salzwedel, Karl
; TITLE OF INVENTION: Method for Detecting Viral Inactivating Agents
```

```

; FILE REFERENCE: 1900.0380001
; CURRENT APPLICATION NUMBER: US/10/685,801
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US 60/418,341
; PRIOR FILING DATE: 2002-10-16
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human Immunodeficiency virus 1
US-10-685-801-47

Query Match          93.4%; Score 185; DB 4; Length 36;
Best Local Similarity 91.7%; Pred. No. 2.2e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESNQOEKNEQELLELDKWSLWNWF 36
   |||:|||||:|||||:|||||:|||||:|||||
Db 1 YTSEIYTLLEESNQOEKNEQELLELDKWSLWNWF 36

Search completed: March 6, 2006, 15:50:31
Job time : 94 secs
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:37:45 ; Search time 18.3333 Seconds  
(without alignments)  
188.935 Million cell updates/sec

Title: US-09-809-060A-2  
Perfect score: 198  
Sequence: 1 YNTIYTLLEESQKQKNEQELLELDKWSLWNWF 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	21.2	36	2 D83682	hypothetical prote
2	41	20.7	41	2 S27169	aralkyl-CoA N-acyl
3	39	19.7	46	2 B30474	homeotic protein H
4	39	19.7	50	2 D89372	hypothetical prote
5	39	19.7	50	2 F86472	5.7K hypothetical
6	38	19.2	43	2 S02031	zinc-binding prote
7	38	19.2	50	2 T14888	hypothetical prote
8	37	18.7	41	2 T48342	hypothetical prote
9	36	18.2	24	2 S01808	hemoglobin AII - t
10	36	18.2	30	2 I77411	renin-2 - mouse (f
11	36	18.2	32	2 I46523	troponin T 4f - ra
12	36	18.2	45	2 S01814	hemoglobin BII - t
13	36	18.2	48	2 F85646	hypothetical prote
14	35.5	17.9	49	2 S39857	ribosomal protein
15	35	17.7	30	2 A34461	heat shock protein
16	35	17.7	33	2 A82186	hypothetical prote
17	35	17.7	38	2 I66797	troponin T 3f - ra
18	35	17.7	42	2 T07291	hypothetical prote
19	35	17.7	47	2 A40703	androgen-binding p
20	35	17.7	48	2 S74261	troponin T3f, fast
21	35	17.7	50	2 T06541	probable NADPH-fer
22	34	17.2	39	2 I54059	Na+/K+-exchanging
23	34	17.2	49	2 T06923	high light-inducib
24	33.5	16.9	36	2 A95135	hypothetical prote
25	33.5	16.9	45	2 C82233	hypothetical prote
26	33.5	16.9	47	2 S31005	gene 60 protein -
27	33.5	16.9	47	2 G84063	hypothetical prote
28	33	16.7	26	2 S27170	aralkyl-CoA N-a
29	33	16.7	36	2 A34594	myosin regulatory

30	33	16.7	43	2 S21282	thymosin beta-11 -
31	33	16.7	43	2 H83653	hypothetical prote
32	33	16.7	44	1 RH0503	somatomedin - bo
33	33	16.7	49	2 AG3362	hypothetical prote
34	32.5	16.4	43	2 B83894	hypothetical prote
35	32.5	16.4	46	2 A95010	hypothetical prote
36	32.5	16.4	46	2 C95173	hypothetical prote
37	32.5	16.4	49	2 A37405	androgen-binding p
38	32	16.2	29	2 E64036	hypothetical prote
39	32	16.2	30	2 H70152	hypothetical prote
40	32	16.2	39	2 C95128	hypothetical prote
41	32	16.2	42	2 T13295	hypothetical prote
42	32	16.2	43	2 T07503	hypothetical prote
43	32	16.2	44	2 E95248	hypothetical prote
44	32	16.2	44	2 C34327	troponin T, fast s
45	32	16.2	45	1 EABP59	early protein gp5

ALIGNMENTS

RESULT 1

D83682  
hypothetical protein BH0260 [imported] - Bacillus halodurans (strain C-125)  
C;Species: Bacillus halodurans  
C;Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C;Accession: D83682  
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran  
Nucleic Acids Res. 28, 4317-4331, 2000  
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A;Reference number: A83650; MUID:20512582; PMID:11058132  
A;Accession: D83682  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-36 <STO>  
A;Cross-references: UNIPROT:Q9KG53; UNIPARC:UPI0000139521; GB:AP001507; GB:BA000004; NID  
A;Experimental source: strain C-125  
C;Genetics:  
A;Gene: BH0260

Query Match 21.2%; Score 42; DB 2; Length 36;  
Best Local Similarity 47.6%; Pred. No. 1.1e+02;  
Matches 10; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY	8	LEESQKQKNEQELLELDK 28
		:
DB	4	LVNESWEQQRKKIQLLSDEK 24

RESULT 2

S27169  
aralkyl-CoA N-acyltransferase (EC 2.3.1.-) - bovine (fragment)  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 13-Mar-1997 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: S27169  
R;Kelley, M.; Vessey, D.A.  
Biochem. J. 288, 315-317, 1992  
A;Title: Structural comparison between the mitochondrial aralkyl-CoA and arylacetyl-CoA  
A;Reference number: S27169; MUID:93075097; PMID:1445276  
A;Accession: S27169  
A;Molecule type: protein  
A;Residues: 1-41 <REL>  
A;Cross-references: UNIPROT:Q9T2U9; UNIPARC:UPI000008C6A3  
A;Experimental source: kidney  
C;Keywords: acyltransferase

Query Match 20.7%; Score 41; DB 2; Length 41;  
Best Local Similarity 47.1%; Pred. No. 1.8e+02;  
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY	1	YNTIYTLLEESQKQK 17
DB	23	YNTIYHYSEDLNKQGE 39

```

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F86472
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <STO>
A;Cross-references: UNIPROT:Q9C6E9; UNIPARC:UPI00000A80F1; GB:AE005172; NID:g11386311;
C;Genetics:
A;Map position: 1

Query Match 19.7%; Score 39; DB 2; Length 50;
Best Local Similarity 44.4%; Pred. No. 3.8e+02;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELD 27
Db 20 EESQTESESEDETESD 37

RESULT 6
S02031
zinc-binding protein - rat (tentative sequence) (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-Mar-2000
C;Accession: S02031
R;Brand, I.A.; Heinzel, A.; Kratzin, H.; Soeling, H.D.
Eur. J. Biochem. 177, 561-568, 1988
A;Title: Properties of a 19-kDa Zn(2+)-binding protein and sequence of the Zn(2+)-binding
A;Reference number: S02031; MUID:89064809; PMID:3197718
A;Accession: S02031
A;Molecule type: protein
A;Residues: 1-43 <BRA>
A;Cross-references: UNIPARC:UPI0000176609
C;Superfamily: prothymosin alpha
C;Keywords: zinc

Query Match 19.2%; Score 38; DB 2; Length 43;
Best Local Similarity 38.9%; Pred. No. 4.2e+02;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 8 LLEESQNOQEKNEQELLE 25
Db 2 VVEEENGAESEETAE 19

RESULT 7
T14888
hypothetical protein - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14888
R;Wong, K.K.; McClelland, M.; Stillwell, L.C.; Siak, E.C.; Thurston, S.J.; Saffer, J.D.
Infect. Immun. 66, 3365-3371, 1998
A;Title: Identification and sequence analysis of a 27-kilobase chromosomal fragment con
ovar typhimurium Ltr.
A;Reference number: Z18249; MUID:98298059; PMID:9632606
A;Accession: T14888
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-50 <WON>
A;Cross-references: UNIPROT:O85329; UNIPARC:UPI00000B3232; EMBL:AF060869; NID:g3323584;
C;Genetics:
A;Gene: Y1cC
A;Map position: 92 min
C;Superfamily: probable membrane protein ylaB

Query Match 19.2%; Score 38; DB 2; Length 50;
Best Local Similarity 46.7%; Pred. No. 5e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 2 TWTIYTLLEESQNOQ 16

homeotic protein Hox 1.3 homolog - sheep (fragment)
B30474
N;Alternate names: homeotic protein Ohox-8-1
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 31-Dec-2004
C;Accession: B30474
R;Choi, C.L.; Hudson, P.; Stauder, A.; Pietersz, G.; Brandon, M.
Gene 63, 187-197, 1998
A;Title: Molecular cloning and characterization of ovine homeo-box-containing genes.
A;Reference number: JT0273; MUID:88255866; PMID:2898416
A;Accession: B30474
A;Molecule type: DNA
A;Residues: 1-46 <CHO>
A;Cross-references: UNIPARC:UPI000017A32E
A;Note: the authors translated the codon TCC for residue 3 as Pro, CAG for residue 42 as
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;11-46/Domain: homeobox homology (fragment) <HOX>

Query Match 19.7%; Score 39; DB 2; Length 46;
Best Local Similarity 34.6%; Pred. No. 3.5e+02;
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 3 NTIYTLLEESQNOQEKNEQELLELDK 28
Db 2 NSNYTGEPKRSRTATYTRQVLSLEK 27

RESULT 4
D89972
hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D89972
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89972
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-50 <KUR>
A;Cross-references: UNIPROT:Q99T25; UNIPARC:UPI00000D7729; GB:BA000018; PID:g13701646;
A;Experimental source: strain N315
C;Genetics:
A;Gene: SAS053

Query Match 19.7%; Score 39; DB 2; Length 50;
Best Local Similarity 70.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 QNOQEKNEQS 22
Db 38 QNDQEKNSSE 47

RESULT 5
F86472
5.7K hypothetical protein T3209.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86472
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Huntge, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

```

Db 16 TNTFFSLSEQAQADQ 30  
| | | : | : | : |  
| | | : | : | : |

RESULT 8  
T48342  
hypothetical protein F15A17.240 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48342  
R;Bavan, M.; Terry, N.; Ardiles, W.; Buysschaert, C.; Dasseville, R.; De Clerck, R.; Deswies, H.W.; Rudd S.; Lemcke, K.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, April 2000  
A;Reference number: Z24491  
A;Accession: T48342  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-41 <BEV>  
A;Cross-references: UNIPROT:Q9LYW4; UNIPARC:UPI00000AA77A; EMBL:AL163002  
A;Experimental source: cultivar Columbia; BAC clone F15A17  
C;Genetics:  
A;Map position: 5  
A;Note: F15A17.240

Query Match 18.7%; Score 37; DB 2; Length 41;  
Best Local Similarity 37.5%; Pred.No. 5.2e+02;  
Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 7 TLLEESONQOEKNEQE 22  
| | | : | : | : |  
| | | : | : | : |

Db 22 TLLEGTEEDNQOE 37  
| | | : | : | : |  
| | | : | : | : |

RESULT 9  
S01808  
hemoglobin AII - tube worm (Lamellibrachia sp.) (fragment)  
C;Species: Lamellibrachia sp.  
C;Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C;Accession: S01808  
R;Suzuki, T.; Takagi, T.; Ohta, S.  
Biochem. J. 255, 541-545, 1988  
A;Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably  
A;Reference number: S01807; MUID:89076216; PMID:3202832  
A;Accession: S01808  
A;Molecule type: protein  
A;Residues: 1-24 <SUZ>  
A;Cross-references: UNIPROT:Q9TWS6; UNIPARC:UPI0000017711B  
C;Keywords: oxygen carrier

Query Match 18.2%; Score 36; DB 2; Length 24;  
Best Local Similarity 26.3%; Pred.No. 3.8e+02;  
Matches 5; Conservative 8; Mismatches 2; Indels 4; Gaps 1;

QY 16 QEKNEQELLEDKWASLWN 34  
| | | : | : | : |  
| | | : | : | : |

Db 8 EDREMQML---WANVWS 22  
| | | : | : | : |  
| | | : | : | : |

RESULT 10  
I77411  
renin-2 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Oct-2004  
C;Accession: I77411  
R;Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.W.  
Mol. Cell. Biol. 4, 2321-2331, 1984  
A;Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analysis  
A;Reference number: I57576; MUID:85085936; PMID:6392850  
A;Accession: I77411  
A;Status: preliminary; translated from GB/EMBL/DDBU  
A;Molecule type: DNA  
A;Residues: 1-30 <RES>  
A;Cross-references: UNIPROT:P00796; UNIPARC:UPI0000016C94B; GB:K02801; NID:q200695; PIDN:





\*T 0 1.0

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:31:26 ; Search time 114.667 Seconds  
(without alignments)  
137.945 Million cell updates/sec

Title: US-09-809-060a-2

Perfect score: 198

Sequence: 1 YNTIYTLLESQKQKNEQLLELDKWLWNP 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Genesecp21\*
- 2: Genesecp1980s\*
- 3: Genesecp1990s\*
- 4: Genesecp2000s\*
- 5: Genesecp2001s\*
- 6: Genesecp2002s\*
- 7: Genesecp2003as\*
- 8: Genesecp2003bs\*
- 9: Genesecp2004s\*
- 9: Genesecp2005s\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	36	3 AAY89837	Aay89837 Core poly
2	198	100.0	36	4 AAB54786	Aab54786 HIV antiv
3	198	100.0	36	4 AAB92245	Aab92245 Virus rel
4	198	100.0	36	4 AAB78238	Aab78238 Core poly
5	198	100.0	36	4 AAB78237	Aab78237 Core poly
6	198	100.0	36	4 AAB70180	Aau70180 HIV viral
7	198	100.0	36	4 ABB02830	Abb02830 Viral cor
8	198	100.0	36	4 ABB01245	Abb01245 Viral DP1
9	198	100.0	36	4 ABB01244	Abb01244 Viral DP1
10	198	100.0	36	4 AAU13791	Aau13791 DP178-lik
11	198	100.0	36	4 AAU13790	Aau13790 DP178-lik
12	198	100.0	36	5 AAO18772	Aao18772 HIV gp41
13	198	100.0	36	5 ADE02850	Ade02850 Hybrid po
14	198	100.0	36	5 ADE02716	Ade02716 Hybrid po
15	198	100.0	36	6 ABO10164	Abo10164 HIV1-SF2
16	198	100.0	36	6 ADN06923	Adn06923 Peptide #
17	198	100.0	36	8 ADS87258	Ads87258 HIV-1 gp4
18	198	100.0	36	9 ADY17493	Ady17493 HIV-1 tra
19	193	97.5	36	2 AAR98399	Aar98399 DP-178 ho
20	193	97.5	36	2 AAR98399	Aar98399 DP185 cor
21	193	97.5	36	2 AAU17012	Aau17012 DP-178-lik
22	193	97.5	36	3 AAY89836	Aay89836 Core poly
23	193	97.5	36	4 AAG67040	Aag67040 HIV-1 gp4
24	193	97.5	36	4 AAU14012	Aau14012 DP178 hom

25	187	94.4	36	3 AAY89865	Aay89865 Core poly
26	187	94.4	36	4 AAB78086	Aab78086 Core poly
27	187	94.4	36	4 ABB02524	Abb02524 Viral cor
28	187	94.4	36	4 ABB01073	Abb01073 Viral DP1
29	187	94.4	36	4 AAU13619	Aau13619 DP178-lik
30	187	94.4	36	5 ADE02544	Ade02544 Hybrid po
31	187	94.4	48	8 ADU80507	Adu80507 Transmemb
32	187	94.4	48	9 ADZ40285	Adz40285 HIV-1 gp4
33	185	93.4	36	3 AAY89446	Aay89446 Core poly
34	185	93.4	36	3 AAB14575	Aab14575 HIV-1 iso
35	185	93.4	36	4 AAG63902	Aag63902 Amino aci
36	185	93.4	36	4 AAB77847	Aab77847 Core poly
37	185	93.4	36	4 AAU70678	Aau70678 HIV viral
38	185	93.4	36	4 ABB00854	Abb00854 Viral DP1
39	185	93.4	36	4 ABB02329	Abb02329 Viral cor
40	185	93.4	36	4 AAU13400	Aau13400 DP178-lik
41	185	93.4	36	5 ADE02349	Ade02349 Hybrid po
42	185	93.4	36	8 ADN46089	Adn46089 C-helical
43	185	93.4	36	9 ADY29992	Ady29992 HIV-1 gro
44	185	93.4	46	3 AAB14573	Aab14573 HIV-1 iso
45	185	93.4	46	4 AAG63900	Aag63900 Amino aci

## ALIGNMENTS

## RESULT 1

AAAY89837	ID	AAAY89837 standard; peptide; 36 AA.
XX	AC	AAAY89837;
XX	DT	23-MAY-2000 (first entry)
XX	DE	Core polypeptide fragment T No. 1406.
XX	KW	Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;
KW	KW	HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;
KW	KW	anti-fusogenic; differentiation factor; interleukin; interferon;
KW	KW	colony stimulating factor; hormone; angiogenic factor.
XX	OS	Unidentified.
XX	PN	WO9595615-A1.
XX	PD	25-NOV-1999.
XX	PF	20-MAY-1999; 99WO-US011219.
XX	PR	20-MAY-1998; 98US-00082279.
XX	PA	(TRIM-) TRIMERIS INC.
XX	PI	Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
XX	PT	WPI; 2000-136792/12.
XX	PT	A new hybrid polypeptide with enhanced pharmacokinetic properties
XX	PT	comprises enhancer sequence.
XX	PS	Disclosure; Page 45; 124pp; English.
XX	CC	The invention relates to hybrid polypeptides comprising enhancer peptide
XX	CC	sequence linked to core polypeptides. The enhancer polypeptides are
XX	CC	derived from various retroviral envelope (gp41) protein sequences,
XX	CC	especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the
XX	CC	pharmacokinetic properties such as increasing the half-life of any core
XX	CC	polypeptide that they are linked to. The core polypeptides are any
XX	CC	polypeptide that may be introduced into a living system and that can
XX	CC	function as a pharmacologically useful peptide for the treatment or
XX	CC	prevention of a disease. The core polypeptides are bioactive peptides
XX	CC	selected from a growth factor, cytokine, differentiation factor,
XX	CC	interleukin, interferon, colony stimulating factor, hormone or angiogenic

CC factor. The peptides of the invention can be used for inhibiting viral  
CC infection and can be used in anti-viral and anti-fusogenic treatments.  
CC Sequences AY8651-Y9055 represent core polypeptide fragments that can  
CC be used in the invention. Some sequences among those indicated also  
CC comprise enhancer fragments at terminal ends and form hybrid polypeptides  
XX  
XX

SQ Sequence 36 AA;

Query Match 100.0%; Score 198; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36  
|||||  
Db 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36

RESULT 2  
AAB54786  
ID AAB54786 standard; peptide; 36 AA.

AC AAB54786;

XX

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

XX HIV antiviral activity exhibiting peptide SEQ ID NO:3.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;  
KW antifusogenic; mobile blood component; measles virus; MeV; SIV;  
KW simian immunodeficiency virus; human parainfluenza virus; HPiV; RSV;  
KW human respiratory syncytial virus; human immunodeficiency virus; HIV.  
XX  
XX

OS Human immunodeficiency virus 1.

XX

PN WO200069902-A1.

XX

PD 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US013651.

XX

PR 17-MAY-1999; 99US-0134406P.

XX

PR 10-SEP-1999; 99US-0153406P.

XX

XX (CONJ-) CONJUCHEM INC.

XX

PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;

XX

XX WPI; 2001-007496/01.

XX

XX A modified peptide and a reactive group which is reactive with amino

XX groups, hydroxyl groups, or thiol groups on blood components to form

XX stable covalent bonds useful for treatment of viral infections, e.g.

XX human immunodeficiency virus.

XX

XX Claim 6; Page 173; 21pp; English.

CC The present invention describes a modified anti-viral peptide (I)  
CC comprising a peptide that exhibits anti-viral activity and a reactive  
CC group which is reactive with amino groups, hydroxyl groups, or thiol  
CC groups on blood components to form stable covalent bonds. (I) has anti-  
CC viral and anti-fusogenic activities. (I) inhibits viral infection of  
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce  
CC the level of membrane fusion events between two or more entities, e.g.,  
CC virus-cell or cell-cell, relative to the level of membrane fusion that  
CC occurs in the absence of the peptide. (I) is useful in the treatment of  
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPiV,  
CC MeV, and SIV. (I) may be administered prophylactically to previously  
CC uninfected individuals. This is useful in cases where an individual has  
CC been subjected to a high risk of exposure to a virus. By bonding of long-  
CC lived components of the blood, such as immunoglobulin, serum albumin, red  
CC blood cells and platelets the activity is extended for days to weeks.  
CC This is due to improved stability in vivo and a reduced susceptibility to

CC peptidase or protease degradation. This minimises the need for more  
CC frequent, or even continual, administration of the peptides. AAB54784 to  
CC AAB55431 represent peptides used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36  
|||||  
Db 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36

RESULT 3  
AAB92245  
ID AAB92245 standard; peptide; 36 AA.

AC AAB92245;

XX

DT 22-JUN-2001 (first entry)

DT

XX Virus related peptide SEQ ID NO:1421.

XX

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;

XX blood component; modification; succinimidy; maleimido group; amino;

XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX

XX WO200069900-A2.

XX

XX 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US013576.

XX

PR 17-MAY-1999; 99US-0134406P.

XX

PR 10-SEP-1999; 99US-0153406P.

XX

PR 15-OCT-1999; 99US-0159783P.

XX

XX (CONJ-) CONJUCHEM INC.

XX

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX

XX WPI; 2001-112059/12.

XX

XX Modifying and attaching therapeutic peptides to albumin prevents

XX peptidase degradation, useful for increasing length of in vivo activity.

CC peptidase or protease degradation. This minimises the need for more  
CC frequent, or even continual, administration of the peptides. AAB54784 to  
CC AAB55431 represent peptides used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36  
|||||  
Db 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36

RESULT 3  
AAB92245  
ID AAB92245 standard; peptide; 36 AA.

AC AAB92245;

XX

DT 22-JUN-2001 (first entry)

DT

XX Virus related peptide SEQ ID NO:1421.

XX

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;

XX blood component; modification; succinimidy; maleimido group; amino;

XX hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX

XX WO200069900-A2.

XX

XX 23-NOV-2000.

XX

PF 17-MAY-2000; 2000WO-US013576.

XX

PR 17-MAY-1999; 99US-0134406P.

XX

PR 10-SEP-1999; 99US-0153406P.

XX

PR 15-OCT-1999; 99US-0159783P.

XX

XX (CONJ-) CONJUCHEM INC.

XX

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX

XX WPI; 2001-112059/12.

XX

XX Modifying and attaching therapeutic peptides to albumin prevents

XX peptidase degradation, useful for increasing length of in vivo activity.

Query Match 100.0%; Score 198; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKNEQKNEQELLELDKWSLWNWF 36  
 DB 1 YNTIYTLLESQKNEQKNEQELLELDKWSLWNWF 36

RESULT 4  
 AAB78238  
 ID AAB78238 standard; peptide; 36 AA.  
 XX AAB78238;  
 AC AAB78238;  
 DT 19-APR-2001 (first entry)  
 DE Core polypeptide T1406.  
 XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;  
 KW antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;  
 KW fusion-related disorder; bacterial infection; viral infection.  
 XX Unidentified.  
 OS WO200103723-A1.  
 XX 18-JAN-2001.  
 XX 10-JUL-2000; 2000WO-US018772.  
 XX 09-JUL-1999; 99US-00350641.  
 XX (TRIM-) TRIMERIS INC.  
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI; 2001-147136/15.  
 XX  
 XX New hybrid polypeptide, useful for preventing, treating and diagnosing  
 PT e.g. viral infections, comprises an enhancer peptide linked to a core  
 PT polypeptide.  
 XX Disclosure; Page 58; 151pp; English.

CC The present sequence is a core polypeptide which may be linked to an  
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of the  
 CC core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving coiled-  
 CC coil peptide interactions. Other uses include preventing, treating and/or  
 CC diagnosing disorders involving fusion events (e.g. modulation of  
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes  
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral  
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral  
 CC infections caused by human immunodeficiency virus, respiratory syncytial  
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and  
 CC polio virus). The enhancer peptide sequence increases the half-life and  
 CC reduces the clearance rate of therapeutic peptides, which increases their  
 CC efficacy and minimises the incidence and severity of adverse side  
 CC effects. In addition, this increases the sensitivity of the diagnostic  
 CC procedure in which they are used

SQ Sequence 36 AA;  
 Query Match 100.0%; Score 198; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKNEQKNEQELLELDKWSLWNWF 36

DB 1 YNTIYTLLESQKNEQKNEQELLELDKWSLWNWF 36

RESULT 5  
 AAB78237  
 ID AAB78237 standard; peptide; 36 AA.  
 XX AAB78237;  
 AC AAB78237;  
 DT 19-APR-2001 (first entry)  
 DE Core polypeptide T1405.  
 XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;  
 KW antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;  
 KW fusion-related disorder; bacterial infection; viral infection.  
 XX Unidentified.  
 OS WO200103723-A1.  
 XX 18-JAN-2001.  
 XX 10-JUL-2000; 2000WO-US018772.  
 XX 09-JUL-1999; 99US-00350641.  
 XX (TRIM-) TRIMERIS INC.  
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI; 2001-147136/15.  
 XX  
 XX New hybrid polypeptide, useful for preventing, treating and diagnosing  
 PT e.g. viral infections, comprises an enhancer peptide linked to a core  
 PT polypeptide.  
 XX Disclosure; Page 58; 151pp; English.

CC The present sequence is a core polypeptide which may be linked to an  
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of the  
 CC core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving coiled-  
 CC coil peptide interactions. Other uses include preventing, treating and/or  
 CC diagnosing disorders involving fusion events (e.g. modulation of  
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes  
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral  
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral  
 CC infections caused by human immunodeficiency virus, respiratory syncytial  
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and  
 CC polio virus). The enhancer peptide sequence increases the half-life and  
 CC reduces the clearance rate of therapeutic peptides, which increases their  
 CC efficacy and minimises the incidence and severity of adverse side  
 CC effects. In addition, this increases the sensitivity of the diagnostic  
 CC procedure in which they are used

SQ Sequence 36 AA;  
 Query Match 100.0%; Score 198; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKNEQKNEQELLELDKWSLWNWF 36  
 DB 1 YNTIYTLLESQKNEQKNEQELLELDKWSLWNWF 36

RESULT 6  
 AAU70180

ID AAU70180 standard; peptide; 36 AA.  
 AC AAU70180;  
 XX  
 DT 14-FEB-2002 (first entry)  
 DE  
 XX HIV viral envelope protein stabilising peptide #2.  
 DE  
 XX Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;  
 KW anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;  
 KW alpha-helical region; ectodomain.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200170262-A2.  
 PN  
 XX 27-SEP-2001.  
 PD  
 XX 15-MAR-2001; 2001WO-US008108.  
 PF  
 XX 17-MAR-2000; 2000US-0189981P.  
 PR  
 XX (PANA-) PANACOS PHARM INC.  
 PA  
 XX Wild CT, Allaway GP;  
 XX WPI; 2001-626098/72.  
 DR  
 XX Immunogenic composition for inhibiting HIV infection, comprises viral  
 PT envelope protein or its fragment exterior to viral membrane, a  
 PT stabilising peptide, and, optionally, viral cell surface receptor or its  
 PT fragment.  
 XX  
 PS Claim 6; Page 45; 84pp; English.  
 XX  
 CC The invention relates to methods of generating immunogens that elicit  
 CC neutralising antibodies which target regions of viral envelope proteins  
 CC such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-  
 CC 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and  
 CC AAU70677-AAU70743 represent stabilising peptides modelling the alpha-  
 CC helical regions of the ectodomain of the HIV-1 transmembrane protein to  
 CC stabilise fusion-active intermediate structures, which can be used as  
 CC vaccine immunogens. Immunogenic compositions comprise a viral envelope  
 CC protein or its fragment exterior to the viral membrane, a stabilising  
 CC peptide to disrupt formation of structural intermediates necessary for  
 CC viral fusion and entry, and optionally, a viral cell surface receptor or  
 CC its fragment. The stabilising peptide is capable of associating with the  
 CC envelope protein or its fragment to form a stabilised, fusion active  
 CC structure. Antibody binding assays are used to determine the ability of  
 CC immunogen vaccines to generate an immune response to various forms of  
 CC envelope. Virus neutralisation assays can be used to characterise the  
 CC antibody response raised against HIV-1 gp41 domains. The sequences and  
 CC methods are useful for inhibiting HIV infection, for inducing an immune  
 CC response in an animal and for raising antibodies  
 XX  
 SQ Sequence 36 AA;  
 Query Match 100.0%; Score 198; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YNTNTIYTLLEESQNOQKNEQELLELDKWSLWNWF 36  
 Db 1 YNTNTIYTLLEESQNOQKNEQELLELDKWSLWNWF 36  
 RESULT 7  
 ABB02830  
 ID ABB02830 standard; peptide; 36 AA.  
 XX  
 AC ABB02830;  
 XX  
 DT 11-SEP-2003 (revised)

DT 06-AUG-2003 (revised)  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Viral core polypeptide, SEQ ID NO: 1357.  
 XX  
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.  
 XX  
 OS Viruses.  
 XX  
 PN WO200164013-A2.  
 XX  
 XX 07-SEP-2001.  
 PD  
 XX 07-FEB-2001; 2001WO-US003988.  
 PF  
 XX 29-FEB-2000; 2000US-00515965.  
 PR  
 XX (TRIM-) TRIMERIS INC.  
 PA  
 XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI; 2001-514829/56.  
 DR  
 XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection.  
 XX  
 PS Disclosure; Page 524; 587pp; English.  
 XX  
 CC The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
 CC regions of proteins interact non-covalently with each other and/or with  
 CC peptides derived from them. This interaction is required for normal  
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
 CC peptide analogues may be used to inhibit respiratory syncytial virus  
 CC (RSV) infection in a cell. They may also be used to inhibit HIV  
 CC infection. The present sequence is a peptide provided in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
 CC 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 36 AA;  
 Query Match 100.0%; Score 198; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YNTNTIYTLLEESQNOQKNEQELLELDKWSLWNWF 36  
 Db 1 YNTNTIYTLLEESQNOQKNEQELLELDKWSLWNWF 36  
 RESULT 8  
 ABB01245  
 ID ABB01245 standard; peptide; 36 AA.  
 XX  
 AC ABB01245;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 06-AUG-2003 (revised)  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE Viral DP178/107-like region peptide T1406.  
 XX  
 XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.  
 XX  
 OS Viruses.

PN WO200164013-A2.  
XX  
PD 07-SEP-2001.  
XX  
PF 07-FEB-2001; 2001WO-US003988.  
XX  
PR 29-FEB-2000; 2000US-00515965.  
XX  
XX (TRIM-) TRIMERIS INC.  
PA  
XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
XX WPI; 2001-514829/56.  
XX  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection.  
XX  
XX Disclosure; Page 58; 587pp; English.  
XX  
CC The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
CC regions of proteins interact non-covalently with each other and/or with  
CC peptides derived from them. This interaction is required for normal  
CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
CC peptide analogues may be used to inhibit respiratory syncytial virus  
CC (RSV) infection in a cell. They may also be used to inhibit HIV  
CC infection. The present sequence is a peptide provided in the  
CC specification. (Updated on 08-AUG-2003 to correct OS field.) (Updated on  
CC 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 36 AA;  
  
Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YNTVTYTLLESQNOQEKNEQELLELDKWASLWNWF 36  
DB 1 YNTVTYTLLESQNOQEKNEQELLELDKWASLWNWF 36  
  
RESULT 9  
ABB01244  
ID ABB01244 standard; peptide; 36 AA.  
XX  
AC ABB01244;  
XX  
XX 11-SEP-2003 (revised)  
DT 06-AUG-2003 (revised)  
DT 03-JAN-2002 (first entry)  
XX  
XX Viral DP178/107-like region peptide T1405.  
DE  
XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
KW infection.  
XX  
OS Viruses.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1  
FT /note= "N-terminal is substituted by Ac"  
FT Modified-site 36  
FT /note= "C-terminal amide"  
XX  
XX WO200164013-A2.  
PN  
XX  
PD 07-SEP-2001.  
XX  
XX 07-FEB-2001; 2001WO-US003988.  
PF

XX 29-FEB-2000; 2000US-00515965.  
PR (TRIM-) TRIMERIS INC.  
XX  
XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
XX WPI; 2001-514829/56.  
XX  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection.  
XX  
XX Disclosure; Page 58; 587pp; English.  
XX  
CC The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
CC regions of proteins interact non-covalently with each other and/or with  
CC peptides derived from them. This interaction is required for normal  
CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
CC peptide analogues may be used to inhibit respiratory syncytial virus  
CC (RSV) infection in a cell. They may also be used to inhibit HIV  
CC infection. The present sequence is a peptide provided in the  
CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
CC 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 36 AA;  
  
Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YNTVTYTLLESQNOQEKNEQELLELDKWASLWNWF 36  
DB 1 YNTVTYTLLESQNOQEKNEQELLELDKWASLWNWF 36  
  
RESULT 10  
AAU13791  
ID AAU13791 standard; peptide; 36 AA.  
XX  
AC AAU13791;  
XX  
XX 21-NOV-2001 (first entry)  
DT  
XX DP178-like/DP107-like peptide T-1406.  
DE  
XX  
XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
KW antifusogenic; antiviral; HIV transmission; mutant; mutein.  
XX  
XX Human immunodeficiency virus 1; isolate LAI.  
OS Synthetic.  
XX  
XX WO200151673-A2.  
PN  
XX 19-JUL-2001.  
PD  
XX 05-JUL-2000; 2000WO-US035727.  
PF  
XX 09-JUL-1999; 99US-00350841.  
PR (TRIM-) TRIMERIS INC.  
XX  
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
PI WPI; 2001-442157/47.  
XX  
XX Identifying a compound that inhibits the formation of or disrupts a  
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
PT or intracellular modulatory activity, by detecting the formation of a  
PT DP107/DP178 complex.

XX PS Disclosure; Page 77; 259pp; English.

CC The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifuogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The present sequence represents one of the DP178-like/DP107-like peptides of the invention

XX SQ Sequence 36 AA;

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36  
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 11

AAU13790

ID AAU13790 standard; peptide; 36 AA.

XX AC AAU13790;

XX 21-NOV-2001 (first entry)

XX DP178-like/DP107-like peptide T-1405.

XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41; antifuogenic; antiviral; HIV transmission; mutant; mutein.

XX Human immunodeficiency virus 1; isolate LAI.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal is substituted by Ac"

FT Modified-site 36 /note= "C-terminal amide"

FT

XX WO200151673-A2.

XX 19-JUL-2001.

XX 05-JUL-2000; 2000WO-US035727.

XX 09-JUL-1999; 99US-00350841.

XX (TRIM-) TRIMERIS INC.

XX Jeffe P, Lackey JW, Erickson JB, Lawless MK, Merutka G;

XX WPI; 2001-442157/47.

XX Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifuogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DP107/DP178\*complex!

XX Disclosure; Page 77; 259pp; English.

XX CC The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifuogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The present sequence represents one of the DP178-like/DP107-like peptides of the invention

XX SQ Sequence 36 AA;

Query Match 100.0%; Score 198; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36  
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 12

AAO18772

ID AAO18772 standard; peptide; 36 AA.

XX AC AAO18772;

XX 29-OCT-2002 (first entry)

XX HIV gp41 protein DP-178 region derived peptide SEQ ID NO: 3.

XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107; gp41.

XX Human immunodeficiency virus.

XX WO200256902-A2.

XX 25-JUL-2002.

XX 17-DEC-2001; 2001WO-US048802.

XX 19-DEC-2000; 2000US-0256657P.

XX (SCHE ) SCHERING CORP.

XX Baroudy BM;

XX WPI; 2002-636513/68.

XX Treatment of HIV infection in an individual involves administration of a combination of chemokine co-receptor five antagonist and a specified HIV envelope polypeptide.

XX Disclosure; Page 32; 52pp; English.

XX The present invention relates to a method of treating an HIV infection in an individual, which involves administering in combination a chemokine co-receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its derivative. Other viral infections can also be treated using the method. The present sequence is a peptide derived from HIV and useful in the method of the invention

XX SQ Sequence 36 AA;

Query Match 100.0%; Score 198; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36  
|||||  
DB 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36  
|||||

## RESULT 13

ADE02850  
ID ADE02850 standard; peptide; 36 AA.

XX AC ADE02850;

DT 29-JAN-2004 (first entry)

XX Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1357.

XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;

XX pharmacokinetic; fusogenic; insulin; diabetes.

XX Unidentified.

XX US6348568-B1.

XX 19-FEB-2002.

XX 20-MAY-1999; 99US-00315304.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2002-424396/45.

XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral  
PT activity, has enhancer peptide sequence derived from retroviral envelope  
PT protein sequences linked to core polypeptide e.g. therapeutic protein.

XX Disclosure; SEQ ID NO 1357; 70pp; English.

XX The invention relates to a novel hybrid polypeptide comprising an  
CC enhancer peptide sequence linked to a core polypeptide. The enhancer  
CC peptide sequence comprises WOEWQKI or WASLWFW. The invention also  
CC includes novel peptides that exhibit anti-fusogenic activity, antiviral  
CC activity and/or ability to modulate intracellular processes. The novel  
CC hybrid polypeptide has virucide and antidiabetic activity. The enhancer  
CC peptide sequence enhances pharmacokinetic properties of any core  
CC polypeptide, for example, a polypeptide useful for the treatment or  
CC prevention of a disease, or an imaging agent useful for imaging  
CC structures in vivo. The core polypeptides and hybrid polypeptides are  
CC useful for modulating fusogenic events and exhibit antifusogenic or  
CC antiviral activity. The novel hybrid polypeptide is useful for decreasing  
CC viral infection and modulating intracellular processes involving coiled-  
CC coil peptide interactions. The novel hybrid polypeptide comprises insulin  
CC or its fragment, so the core polypeptide is useful for ameliorating the  
CC symptoms of forms of diabetes. The novel hybrid polypeptide is also  
CC useful as a part of prognosis for preventing disorders including fusion  
CC events and viral infection that involves cell-cell and/or virus-cell  
CC fusion, and for diagnosis and in vivo imaging methods. This sequence  
CC represents an enhancer peptide of the invention.

XX Sequence 36 AA;

Query Match 100.0%; Score 198; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36  
|||||

DB 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36

## RESULT 14

ADE02716  
ID ADE02716 standard; peptide; 36 AA.

XX AC ADE02716;

DT 29-JAN-2004 (first entry)

XX Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID No 1223.

XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;

XX pharmacokinetic; fusogenic; insulin; diabetes.

XX Unidentified.

XX Key Location/Qualifiers

XX Modified-site 1 /note= "Residue is modified by acetyl group"

XX Modified-site 36 /note= "C-terminal amide"

XX US6348568-B1.

XX 19-FEB-2002.

XX 20-MAY-1999; 99US-00315304.

XX 20-MAY-1998; 98US-00082279.

XX (TRIM-) TRIMERIS INC.

XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;

XX WPI; 2002-424396/45.

XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral  
PT activity, has enhancer peptide sequence derived from retroviral envelope  
PT protein sequences linked to core polypeptide e.g. therapeutic protein.

XX Disclosure; SEQ ID NO 1223; 70pp; English.

XX The invention relates to a novel hybrid polypeptide comprising an  
CC enhancer peptide sequence linked to a core polypeptide. The enhancer  
CC peptide sequence comprises WOEWQKI or WASLWFW. The invention also  
CC includes novel peptides that exhibit anti-fusogenic activity, antiviral  
CC activity and/or ability to modulate intracellular processes. The novel  
CC hybrid polypeptide has virucide and antidiabetic activity. The enhancer  
CC peptide sequence enhances pharmacokinetic properties of any core  
CC polypeptide, for example, a polypeptide useful for the treatment or  
CC prevention of a disease, or an imaging agent useful for imaging  
CC structures in vivo. The core polypeptides and hybrid polypeptides are  
CC useful for modulating fusogenic events and exhibit antifusogenic or  
CC antiviral activity. The novel hybrid polypeptide is useful for decreasing  
CC viral infection and modulating intracellular processes involving coiled-  
CC coil peptide interactions. The novel hybrid polypeptide comprises insulin  
CC or its fragment, so the core polypeptide is useful for ameliorating the  
CC symptoms of forms of diabetes. The novel hybrid polypeptide is also  
CC useful as a part of prognosis for preventing disorders including fusion  
CC events and viral infection that involves cell-cell and/or virus-cell  
CC fusion, and for diagnosis and in vivo imaging methods. This sequence  
CC represents an enhancer peptide of the invention.

XX Sequence 36 AA;

Query Match 100.0%; Score 198; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36  
|||||

Search completed: March 6, 2006, 15:37:19  
Job time : 117.667 secs

Db 1 YNTYITVLTLEESQKQEKNEQELLELDKWSLWNWF 36

RESULT 15

ABO10164  
ID ABO10164 standard; peptide; 36 AA.

XX AC ABO10164;

XX 23-OCT-2003 (revised)

DT 19-AUG-2003 (first entry)

XX HIV1-SF2 gp41 protein, DP85 peptide.

XX HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;

KW Epstein-Barr virus infection; heptad repeat motif.

XX Human immunodeficiency virus 1; isolate SF2.

XX US6518013-B1.

XX 11-FEB-2003.

XX 07-JUN-1995; 95US-00485546.

XX 07-JUN-1993; 93US-00073028.

PR 07-JUN-1994; 94US-00255208.

PR 20-DEC-1994; 94US-00360107.

XX (TRIM-) TRIMERIS INC.

XX Barney SO, Lambert DM, Petteway SR;

XX WPI; 2003-465599/44.

PT Inhibiting transmission of Epstein-Barr virus to a cell, by contacting  
the cell with a peptide consisting of a region of Epstein-Barr virus  
protein.

PS Example; Fig 1; 716pp; English.

XX The invention relates to inhibiting (M) transmission of an Epstein-Barr  
virus to a cell, comprising contacting the cell with an effective  
concentration of a peptide consisting of a region of 16-39 consecutive  
amino acids of an Epstein-Barr virus protein for an effective period of  
time, where the region is recognised by one or more of ALLM0115,  
107X178x4 or PLZIP sequence search motifs, the peptide further comprises  
an amino terminal X, and a carboxy terminal Z in which X comprises an  
amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic  
group or macromolecular carrier group, and Z comprises a carboxyl group,  
amido group, hydrophobic group, or macromolecular carrier group, and  
fusion of the virus to the cell is inhibited. The peptides were  
identified by analysing the structure/motifs present in the HIV-1  
glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat  
motif containing peptides were used to design the motifs cited above,  
which in turn were used to analyse proteins from other pathogenic  
organisms and HIV isolates, looking for DP107/178 structural analogues.  
The method is useful for inhibiting transmission of Epstein-Barr virus to  
a cell and Epstein-Barr virus infection. The present sequence is a  
control peptide used in the study of the DP178 structure. (Updated on 23-  
OCT-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 198; DB 6; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITVLTLEESQKQEKNEQELLELDKWSLWNWF 36

Db 1 YNTYITVLTLEESQKQEKNEQELLELDKWSLWNWF 36





```

OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06738; AAA19152.1; -; mRNA.
DR HSSP; P31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6196 MW; E9B618825B832D1E CRC64;

Query Match 91.9%; Score 182; DB 2; Length 49;
Best Local Similarity 91.7%; Pred. No. 5.7e-14;
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db |||||
14 YTGLIYTLLEKSQNOQEKNEQELLELDKWASLWNWF 49

RESULT 3
Q69895_9HIV1
ID Q69895_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69895;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06725; AAA19138.1; -; mRNA.
DR HSSP; P31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6168 MW; 8077C4815B83281E CRC64;

Query Match 89.4%; Score 177; DB 2; Length 49;
Best Local Similarity 91.7%; Pred. No. 2.2e-13;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db |||||
14 YTGLIYTLLEESQIQOQEKNEQELLELDKWASLWNWF 49

RESULT 4
Q69895_9HIV1
ID Q69895_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69895;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06725; AAA19138.1; -; mRNA.
DR HSSP; P31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6168 MW; 8077C4815B83281E CRC64;

Query Match 89.4%; Score 177; DB 2; Length 49;
Best Local Similarity 91.7%; Pred. No. 2.2e-13;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db |||||
14 YTGLIYTLLEESQIQOQEKNEQELLELDKWASLWNWF 49

RESULT 5
Q69906_9HIV1
ID Q69906_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69906;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06736; AAA19149.1; -; mRNA.
DR HSSP; P31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 1
FT NON_TER 49 49
SQ SEQUENCE 49 AA; 6214 MW; 29C4E5A8CDBD63DD8 CRC64;

Query Match 89.4%; Score 177; DB 2; Length 49;
Best Local Similarity 91.7%; Pred. No. 2.2e-13;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db |||||
14 YTGLIYTLLEESQIQOQEKNEQELLELDKWASLWNWF 49
```

DR ENBL; U06729; AAA19142.1; -, mRNA.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 FT NON\_TER 1  
 FT NON\_TER 50  
 SQ SEQUENCE 50 AA; 6287 MW; EABA093F0877D85B CRC64;  
 Query Match 87.4%; Score 173; DB 2; Length 50;  
 Best Local Similarity 86.1%; Pred. No. 8.5e-13;  
 Matches 30; Conservative 2; Mismatches 3; Indels 0; Gaps

Qy 1 YTNNTIYTLLEESQNQOEKNEQELLELDKWSLWNWF 36  
 |||:|||||:|||||:|||||:|||||:|||||:  
 Db 15 YTGVIYTLLEESQNQOEKNEQDILLDKWANLWNWF 50  
 |||:|||||:|||||:|||||:|||||:|||||:

RESULT 8  
 ID Q69907\_9HIV1 PRELIMINARY; PRT; 49 AA.  
 AC Q69907;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE GP41 (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae  
 OC Lentivirus; Primate lentivirus group.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=94211861; PubMed=7512731;  
 RA Conley A.J., Keesler J.A., Boocke L.J., Tung J.S., Arnold B.A.,  
 RA Keller P.M., Shaw A.R., Emini E.A.;  
 RT "Neutralization of divergent human immunodeficiency virus type 1  
 RT variants and primary isolates by IAM-41-3P5, an anti-gp41 human  
 RT monoclonal antibody.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).  
 DR ENBL; U06737; AAA19150.1; -, mRNA.  
 DR HSP; Q87973; 2SIV.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 FT NON\_TER 1  
 FT NON\_TER 49  
 SQ SEQUENCE 49 AA; 6241 MW; 29C4ESA8CBC7CDD8 CRC64;  
 Query Match 86.9%; Score 172; DB 2; Length 49;  
 Best Local Similarity 83.3%; Pred. No. 8.5e-13;  
 Matches 30; Conservative 4; Mismatches 2; Indels 0; Gaps

Qy 1 YTNNTIYTLLEESQNQOEKNEQELLELDKWSLWNWF 36  
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 Db 14 YTSLIYTLLEESQTQOEKNEKELLELDKWANLWNWF 49  
 |||:|||||:|||||:|||||:|||||:|||||:

RESULT 9  
 ID Q69908\_9HIV1 PRELIMINARY; PRT; 49 AA.  
 AC Q69908;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE GP41 (Fragment).  
 GN Name=env;  
 OS Human immunodeficiency virus 1.  
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae  
 OC Lentivirus; Primate lentivirus group.  
 OX NCBI\_TaxID=11676;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=94211861; PubMed=7512731;  
 RA Conley A.J., Keesler J.A., Boocke L.J., Tung J.S., Arnold B.A.,  
 RA Keller P.M., Shaw A.R., Emini E.A.;  
 RT "Neutralization of divergent human immunodeficiency virus type 1  
 RT variants and primary isolates by IAM-41-3P5, an anti-gp41 human  
 RT monoclonal antibody.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).  
 DR ENBL; U06737; AAA19150.1; -, mRNA.  
 DR HSP; Q87973; 2SIV.  
 DR GO; GO:0016021; C:integral to membrane; IEA.  
 DR GO; GO:0019031; C:viral envelope; IEA.  
 DR GO; GO:0005198; F:structural molecule activity; IEA.  
 DR InterPro; IPR000328; Env\_GP41.  
 DR Pfam; PF00517; GP41; 1.  
 FT NON\_TER 1  
 FT NON\_TER 49  
 SQ SEQUENCE 49 AA; 6241 MW; 29C4ESA8CBC7CDD8 CRC64;  
 Query Match 86.9%; Score 172; DB 2; Length 49;  
 Best Local Similarity 83.3%; Pred. No. 8.5e-13;  
 Matches 30; Conservative 4; Mismatches 2; Indels 0; Gaps

OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94211861; PubMed=7512731;  
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,  
Keller P.M., Shaw A.R., Emini E.A.;  
RT "Neutralization of divergent human immunodeficiency virus type 1  
variants and primary isolates by IAM-41-2F5, an anti-gp41 human  
monoclonal antibody";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).  
DR EMBL; U06738; AAA19151.1; -; mRNA.  
DR HSSP; Q87973; 2S1V.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
FT NON\_TER 1 1  
FT NON\_TER 49 49  
SQ SEQUENCE 49 AA; 6283 MW; 74CD75339B92C172 CRC64;

Query Match 86.9%; Score 172; DB 2; Length 49;  
Best Local Similarity 83.3%; Pred. No. 8.5e-13;  
Matches 30; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YNTNTYTLLEESQKQKNEQELLELDKWASLWNWF 36  
||:|||||:|||||:|||||:|||||:|||||  
Db 14 YTSIIYTLLEKSNQKQKNEKELLELDKWTLNWNF 49

RESULT 10  
Q69905 9HIV1  
ID Q69905\_9HIV1 PRELIMINARY; PRT; 34 AA.  
AC Q69905;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94211861; PubMed=7512731;  
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,  
Keller P.M., Shaw A.R., Emini E.A.;  
RT "Neutralization of divergent human immunodeficiency virus type 1  
variants and primary isolates by IAM-41-2F5, an anti-gp41 human  
monoclonal antibody";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).  
DR EMBL; U06735; AAA19148.1; -; mRNA.  
DR HSSP; F31872; 1LB0.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
FT NON\_TER 1 1  
FT NON\_TER 34 34  
SQ SEQUENCE 34 AA; 4196 MW; 7B724A8EA164BD9C CRC64;

Query Match 86.4%; Score 171; DB 2; Length 34;  
Best Local Similarity 96.9%; Pred. No. 7.4e-13;  
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 IYTLLEESQKQKNEQELLELDKWASLWNWF 36  
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Db 3 IYTLLEKSNQKQKNEQELLELDKWASLWNWF 34

RESULT 11

Q69900 9HIV1  
ID Q69900\_9HIV1 PRELIMINARY; PRT; 50 AA.  
AC Q69900;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94211861; PubMed=7512731;  
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,  
Keller P.M., Shaw A.R., Emini E.A.;  
RT "Neutralization of divergent human immunodeficiency virus type 1  
variants and primary isolates by IAM-41-2F5, an anti-gp41 human  
monoclonal antibody";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).  
DR EMBL; U06730; AAA19143.1; -; mRNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
FT NON\_TER 1 1  
FT NON\_TER 50 50  
SQ SEQUENCE 50 AA; 6300 MW; EABA093F086C79E1 CRC64;

Query Match 84.8%; Score 168; DB 2; Length 50;  
Best Local Similarity 83.3%; Pred. No. 2.6e-12;  
Matches 30; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
QY 1 YNTNTYTLLEESQKQKNEQELLELDKWASLWNWF 36  
||:|||||:|||||:|||||:|||||:|||||  
Db 15 YTGIIYNLEESQKQKNEQELLELDKWALWNWF 50

RESULT 12  
Q69903 9HIV1  
ID Q69903\_9HIV1 PRELIMINARY; PRT; 34 AA.  
AC Q69903;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Gp41 (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94211861; PubMed=7512731;  
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,  
Keller P.M., Shaw A.R., Emini E.A.;  
RT "Neutralization of divergent human immunodeficiency virus type 1  
variants and primary isolates by IAM-41-2F5, an anti-gp41 human  
monoclonal antibody";  
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).  
DR EMBL; U06733; AAA19146.1; -; mRNA.  
DR HSSP; F31872; 1LB0.  
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DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
FT NON\_TER 1 1  
FT NON\_TER 34 34  
SQ SEQUENCE 34 AA; 4226 MW; E609273F6164BD80 CRC64;

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Query Match      84.3%; Score 167; DB 2; Length 34;
Best Local Similarity 93.8%; Pred. No. 2.2e-12;
Matches 30; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 3 IYTLLESQOQEKNEQELLELDKWASLWNWF 34

RESULT 13
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ID Q69893_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69893;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06723; AAA19136.1; -; mRNA.
DR HSSP; P31872; ILBO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 34 34
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4196 MW; 0C7CAA60A164B89C CRC64;

Query Match      83.8%; Score 166; DB 2; Length 34;
Best Local Similarity 96.9%; Pred. No. 2.9e-12;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IYTLLESQOQEKNEQELLELDKWASLWNWF 36
   |||||:|||||:|||||:|||||:|||||
Db 3 IYTLLESQOQEKNEQELLELDKWASLWNWF 34

RESULT 14
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ID Q69894_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69894;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
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DR EMBL; U06724; AAA19137.1; -; mRNA.
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DR GO; GO:0005198; F:structural molecule activity; IEA.
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DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 1
FT NON_TER 34 34
FT NON_TER 34 34
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Db 3 IYTLLESQOQEKNEQELLELDKWASLWNWF 34

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ID Q69904_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69904;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06734; AAA19147.1; -; mRNA.
DR HSSP; P31872; ILBO.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 1
FT NON_TER 34 34
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4184 MW; BB1CAA65F131AD5A CRC64;

Query Match      82.3%; Score 163; DB 2; Length 34;
Best Local Similarity 90.6%; Pred. No. 6.5e-12;
Matches 29; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 IYTLLESQOQEKNEQELLELDKWASLWNWF 36
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Db 3 IYTLLESQOQEKNEQELLELDKWASLWNWF 34

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Job time : 118.667 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 15:43:35 ; Search time 27.6667 Seconds  
(without alignments)  
107.578 Million cell updates/sec

Title: US-09-809-060A-2

Perfect score: 198

Sequence: 1 YNTIYTLLEESQKNEQELLELDKWLWNP 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	198	100.0	36	2 US-08-484-223B-3	Sequence 3, Appli
3	198	100.0	36	2 US-08-919-597-3	Sequence 3, Appli
4	198	100.0	36	2 US-08-475-668A-3	Sequence 3, Appli
5	198	100.0	36	2 US-08-485-551A-3	Sequence 3, Appli
6	198	100.0	36	2 US-08-471-913A-3	Sequence 3, Appli
7	198	100.0	36	2 US-08-485-264A-3	Sequence 3, Appli
8	198	100.0	36	2 US-09-082-279B-1357	Sequence 1357, Ap
9	198	100.0	36	2 US-08-474-349A-3	Sequence 3, Appli
10	198	100.0	36	2 US-09-315-304B-1357	Sequence 1357, Ap
11	198	100.0	36	2 US-08-255-208A-3	Sequence 3, Appli
12	198	100.0	36	2 US-08-973-952-3	Sequence 3, Appli
13	198	100.0	36	2 US-08-470-896-3	Sequence 3, Appli
14	198	100.0	36	2 US-08-485-546A-3	Sequence 3, Appli
15	198	100.0	36	2 US-09-834-784-1357	Sequence 1357, Ap
16	198	100.0	36	2 US-09-515-965A-1357	Sequence 1357, Ap
17	198	100.0	36	2 US-09-350-641C-1357	Sequence 1357, Ap
18	198	100.0	36	2 US-09-350-841A-1357	Sequence 1357, Ap
19	198	100.0	36	2 US-08-487-266A-3	Sequence 3, Appli
20	198	100.0	36	2 US-09-623-548A-1421	Sequence 1421, Ap
21	198	100.0	36	2 US-10-252-136-3	Sequence 3, Appli
22	198	100.0	36	2 US-09-657-276-1421	Sequence 1421, Ap
23	198	100.0	36	2 US-08-484-741-3	Sequence 3, Appli
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25	193	97.5	36	2 US-08-360-107A-3	Sequence 3, Appli
26	193	97.5	36	2 US-08-554-616-3	Sequence 3, Appli
27	193	97.5	36	2 US-09-350-841A-1543	Sequence 1543, Ap

Query Match 100.0%; Score 198; DB 2; Length 36;

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32 187 94.4 36 2 US-09-350-641C-1051 Sequence 1051, Ap  
33 187 94.4 36 2 US-09-350-841A-1051 Sequence 1051, Ap  
34 185 93.4 36 2 US-09-082-279B-856 Sequence 856, App  
35 185 93.4 36 2 US-09-315-304B-856 Sequence 856, App  
36 185 93.4 36 2 US-09-834-784-856 Sequence 856, App  
37 185 93.4 36 2 US-09-779-451-47 Sequence 47, Appl  
38 185 93.4 36 2 US-09-515-965A-856 Sequence 856, App  
39 185 93.4 36 2 US-09-350-641C-856 Sequence 856, App  
40 185 93.4 36 2 US-09-350-841A-856 Sequence 856, App  
41 185 93.4 46 2 US-09-779-451-45 Sequence 109, Appl  
42 183 92.4 46 2 US-08-965-056-109 Sequence 109, Appl  
43 181 91.4 36 2 US-09-082-279B-642 Sequence 642, App  
44 181 91.4 36 2 US-09-315-304B-642 Sequence 642, App  
45 181 91.4 36 2 US-09-834-784-642 Sequence 642, App

## ALIGNMENTS

## RESULT 1

US-08-486-099-3  
; Sequence 3, Application US/08486099  
; Patent No. 6013263

## GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
TITLE OF INVENTION: B VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 209  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,099  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

## INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-486-099-3

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Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36
Db 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36

RESULT 2
US-08-484-223B-3
; Sequence 3, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-484-223B-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36
Db 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36

RESULT 3
US-08-919-597-3
; Sequence 3, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
```

```
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-919-597-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36
Db 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36

RESULT 4
US-08-475-668A-3
; Sequence 3, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
```



COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-3

Query Match 100.0%; Score 198; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36  
|||  
DB 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36

## RESULT 5

US-08-485-551A-3  
Sequence 3, Application US/08485551A  
Patent No. 6068973  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,551A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-023  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-485-551A-3

Query Match 100.0%; Score 198; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36  
|||  
DB 1 YNTIYTLLESQKQKNEQELLELDKWSLWNWF 36

## RESULT 6

US-08-471-913A-3  
Sequence 3, Application US/08471913A  
Patent No. 6093794  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 214  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,913A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-471-913A-3

Query Match 100.0%; Score 198; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQKQKNEQELLELDKWASLWNWF 36  
|||||  
Db 1 YNTNTYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 7  
US-08-485-264A-3  
; Sequence 3, Application US/08485264A  
; Patent No. 6228983  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
; NUMBER OF SEQUENCES: 232  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,264A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-021  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-485-264A-3

Query Match 100.0%; Score 198; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQKQKNEQELLELDKWASLWNWF 36  
|||||  
Db 1 YNTNTYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 8  
US-09-082-279B-1357  
; Sequence 1357, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Marutka, Gene  
; APPLICANT: Anwer, Mohmed  
; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082,279B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1357  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-082-279B-1357

Query Match 100.0%; Score 198; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.3e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTNTYTLLEESQKQKNEQELLELDKWASLWNWF 36  
|||||  
Db 1 YNTNTYTLLEESQKQKNEQELLELDKWASLWNWF 36

RESULT 9  
US-08-474-349A-3  
; Sequence 3, Application US/08474349A  
; Patent No. 6333395  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA  
; NUMBER OF SEQUENCES: 517  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,349A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-474-349A-3

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Query Match      100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 10
US-09-315-304B-1357
; Sequence 1357, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1357
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-315-304B-1357

Query Match      100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 11
US-08-255-208A-3
; Sequence 3, Application US/08255208A
; Patent No. 6440656
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway Jr., Stephen R.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; FILE REFERENCE: TRANSMISSION
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/255,208A
```

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; FILING DATE: 07-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-255-208A-3

Query Match      100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 12
US-08-973-952-3
; Sequence 3, Application US/08973952A
; Patent No. 6475491
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER VIRAL INFECTIONS
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/08/973,952A
; CURRENT FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 08/481,957
; EARLIER FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-08-973-952-3

Query Match      100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YNTYITLLEESNQOEKNEQELLELDKWASLWNWF 36

RESULT 13
US-08-470-896-3
; Sequence 3, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; FILE REFERENCE: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
```

```
/ NUMBER OF SEQUENCES: 273
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/470,896
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-020
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-08-470-896-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 14
US-08-485-546A-3
/ Sequence 3 Application US/08485546A
/ Patent No. 6518013
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ APPLICANT: Matthews, Thomas J.
/ APPLICANT: Wild, Carl T.
/ APPLICANT: Barney, Shawn O.
/ APPLICANT: Lambert, Dennis M.
/ APPLICANT: Petteway, Stephen R.
/ APPLICANT: Langlois, Alphonse J.
/ TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
/ TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
/ TITLE OF INVENTION: TRANSMISSION
/ NUMBER OF SEQUENCES: 214
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/485,546A
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/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-028
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 36 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ US-08-485-546A-3

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

RESULT 15
US-09-834-784-1357
/ Sequence 1357, Application US/09834784
/ Patent No. 6562787
/ GENERAL INFORMATION:
/ APPLICANT: Barney, Shawn
/ APPLICANT: Guthrie, Kelly
/ APPLICANT: Merutka, Gene
/ APPLICANT: Anwer, Mohmed
/ APPLICANT: Lambert, Dennis
/ TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
/ TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
/ FILE REFERENCE: 7872-043
/ CURRENT APPLICATION NUMBER: US/09/834,784
/ CURRENT FILING DATE: 2001-04-13
/ PRIOR APPLICATION NUMBER: 09/082,279
/ PRIOR FILING DATE: 1998-05-20
/ NUMBER OF SEQ ID NOS: 1515
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1357
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Core polypeptide
/ US-09-834-784-1357

Query Match 100.0%; Score 198; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36
Db 1 YNTIYTLLEESQNOQEKNEQELLELDKWASLWNWF 36

Search completed: March 6, 2006, 15:45:44
Job time : 28.6667 secs
```

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:31:26 ; Search time 114.667 Seconds

(without alignments)  
137.945 Million cell updates/sec

Title: US-09-809-060A-3

Perfect score: 200

Sequence: 1 YTGIIYNLEESQKQKNEQELLELDKQANLWVWF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A\_Geneseq\_21.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2002s.\*

6: Geneseq2003s.\*

7: Geneseq2003bs.\*

8: Geneseq2004s.\*

9: Geneseq2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	100.0	36	2	AAR67699 DP-178 ho
2	200	100.0	36	2	AAR98400 Peptide c
3	200	100.0	36	2	Aaw17013 DP-178-li
4	200	100.0	36	4	Aab54787 HIV antiv
5	200	100.0	36	4	Aab52246 Virus rel
6	200	100.0	36	4	AAB78239 Core poly
7	200	100.0	36	4	AAB78240 Core poly
8	200	100.0	36	4	Aau70181 HIV viral
9	200	100.0	36	4	Abb02832 Viral cor
10	200	100.0	36	4	Abb02831 Viral cor
11	200	100.0	36	4	AAG67041 HIV-1 gp4
12	200	100.0	36	4	Abb01246 Viral DP1
13	200	100.0	36	4	Abb01247 Viral DP1
14	200	100.0	36	4	Aau13793 DP178-lik
15	200	100.0	36	4	Aau13792 DP178-lik
16	200	100.0	36	4	Aau14013 DP178 hom
17	200	100.0	36	5	Aao18773 HIV gp41
18	200	100.0	36	5	Ade02851 Hybrid po
19	200	100.0	36	5	Ade02852 Hybrid po
20	200	100.0	36	6	Ab010165 HIV1-RF g
21	200	100.0	36	8	Adn06924 Peptide #
22	200	100.0	36	8	AdS87259 HIV-1 gp4
23	200	100.0	36	9	Ady71494 HIV-1 tra
24	185	92.5	48	8	ADu80528 Transmem

25	185	92.5	48	9	ADZ40286	Adz40286 HIV-1 gp4
26	184	92.0	36	2	AAR67698	Aar67698 DP-178 ho
27	184	92.0	36	2	AAR98399	Aar98399 DP185 cor
28	184	92.0	36	2	AAW17012	Aaw17012 DP-178-li
29	184	92.0	36	4	AAG67040	Aag67040 HIV-1 gp4
30	184	92.0	36	4	AAU14012	Aau14012 DP178 hom
31	182	91.0	46	2	AAU22914	Aau22914 SEQ ID NO
32	182	91.0	46	5	ABG68385	Abg68385 HIV envel
33	182	91.0	46	6	ABU57792	Abu57792 Human imm
34	182	91.0	48	8	ADU80508	Adu80508 Transmemb
35	182	91.0	48	8	ADU80513	Adu80513 Transmemb
36	182	91.0	48	8	ADU80527	Adu80527 Transmemb
37	182	91.0	48	9	ADZ40266	Adz40266 HIV-1 gp4
38	182	91.0	48	9	ADZ40271	Adz40271 HIV-1 gp4
39	182	91.0	48	9	ADZ40285	Adz40285 HIV-1 gp4
40	181	90.5	48	8	ADU80507	Adu80507 Transmemb
41	181	90.5	48	9	ADZ40265	Adz40265 HIV-1 gp4
42	180.5	90.2	35	3	AAy89838	Aay89838 Core poly
43	180.5	90.2	35	3	AAy89839	Aay89839 Core poly
44	180	90.0	36	4	AAB77633	Aab77633 Core poly
45	180	90.0	36	4	ABB02115	Abb02115 Viral cor

## ALIGNMENTS

## RESULT 1

AAR67699

ID AAR67699 standard; peptide; 36 AA.

XX AAR67699;

AC AAR67699;

XX AAR67699;

DT 16-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 24-AUG-1995 (first entry)

XX AAR67699;

DE DP-178 homologue derived from HIV-1 RP has antiviral activity.

XX AAR67699;

KW AAR67699;

KW AAR67699;

KW AAR67699;

XX AAR67699;

OS AAR67699;

XX AAR67699;

PN AAR67699;

XX AAR67699;

PD AAR67699;

XX AAR67699;

PF AAR67699;

XX AAR67699;

PR AAR67699;

XX AAR67699;

PA AAR67699;

XX AAR67699;

PI AAR67699;

XX AAR67699;

DR AAR67699;

XX AAR67699;

PT AAR67699;

XX AAR67699;

PS AAR67699;

XX AAR67699;

CC AAR67699;

XX AAR67699;

CC AAR67699;

XX AAR67699;

CC AAR67699;

XX AAR67699;

CC AAR67699;

XX AAR67699;

CC AAR67699;

XX AAR67699;

CC AAR67699;

XX AAR67699;

CC AAR67699;

XX AAR67699;

CC AAR67699;

antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;  
human immunodeficiency virus; transmembrane protein; gp41; alpha helix;  
leucine zipper; DP-185.  
Human immunodeficiency virus; (RF isolate).

Computer search generated synthetic peptides - are inhibitors of HIV transmission.

Example; Fig 1; 182pp; English.

This peptide is isolated from HIV-1 isolate RF, and is a homologue of the peptide DP-178. DP-178 corresponds to amino acids 638 to 673 of the HIV-1 isolate LAI transmembrane protein gp41. It forms a putative alpha helix at the C-terminal end of the gp41 ectodomain, and complexes with DP-107 (corresponds to amino acids 558-595) which contains a leucine zipper motif. The peptides complex via non-covalent protein-protein interactions, and possess anti-viral activity. The peptide inhibits transmission to uninfected cells, and can also be used as type and/or subtype specific diagnostic tools. (Updated on 25-MAR-2003 to correct PN

CC field.) (Updated on 16-OCT-2003 to standardise OS field)  
 XX Sequence 36 AA;

Query Match 100.0%; Score 200; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36  
 |||||  
 Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36

## RESULT 2

AAR98400  
 ID AAR98400 standard; peptide; 36 AA.

XX  
 AC AAR98400;

DT 16-OCT-2003 (revised)  
 DT 17-FEB-1997 (first entry)

XX Peptide corresponding to residues 638-673 of HIV-1(RF) gp41.

XX Antifusogenic activity; antiviral capability; coiled-coil peptide;  
 KW ALLMOTI5; 107x178x4; PLZIP search motif; viral transmission; HIV;  
 KW Influenza virus; hepatitis B virus.

XX Human immunodeficiency virus 1.

XX WO9619495-A1.

PN 27-JUN-1996.

XX 20-DEC-1995; 95WO-US016733.

PR 20-DEC-1994; 94US-00360107.

PR 06-JUN-1995; 95US-00470896.

PA (UYDU-) UNIV DUKE

PA (TRIM-) TRIMERIS INC.

XX Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;

PI Petteway SR, Langlois AJ;

XX WPI; 1996-309517/31.

XX Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an  
 PT isolated peptide recognised by an ALLMOTI5, 107x178x4 or PLZIP sequence  
 PT search motif.

PS Disclosure; Fig 1; 471pp; English.

XX The sequences given in AAR98398-408 represent peptides which exhibit  
 CC antifusogenic activity, antiviral capability and/or the ability to  
 CC modulate intracellular processes involving coiled-coil peptide  
 CC structures. These peptides are recognised by the ALLMOTI5, 107x178x4 and  
 CC PLZIP search motifs. These peptides may be used to inhibit the  
 CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B  
 CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 200; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36  
 |||||  
 Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36

## RESULT 3

AAW17013  
 ID AAW17013 standard; peptide; 36 AA.

XX  
 AC AAW17013;

DT 17-OCT-2003 (revised)  
 DT 01-JUL-1997 (first entry)

XX DP-178-like peptide useful for treatment of HIV infection.

XX HIV; SIV; human; simian immunodeficiency virus; glycoprotein 41;  
 KW transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;  
 KW replication; transmission.

XX Human immunodeficiency virus 1; RF isolate.

XX WO9640191-A1.

PN 19-DEC-1996.

XX 06-JUN-1996; 96WO-US009499.

PR 07-JUN-1995; 95US-00481957.

XX (TRIM-) TRIMERIS INC.

XX Johnson RM, Lambert DM;

XX WPI; 1997-099886/09.

XX Compens. contg. DP-178 or DP-107 in combination with other therapeutic  
 PT agent - useful for treatment of HIV infection, esp. by inhibiting  
 PT replication or transmission of HIV.

PS Disclosure; Fig 1; 84pp; English.

XX AAW17012-W17016 are DP-178 homologues that are useful in the treatment of  
 CC HIV infection. DP-178 is a peptide corresponding to residues 638-673 of  
 CC HIV type 1 glycoprotein 41 (gp41) transmembrane protein. DP-178 and its  
 CC derivatives/homologues are used in combination with a therapeutic agent,  
 CC e.g. a reverse transcriptase, viral protease, cytokine, glycosylation or  
 CC viral mRNA processing inhibitor or a nucleoside inhibitor. The peptides  
 CC work by inhibiting viral replication or inhibiting transmission. They may  
 CC also be used in vaccines for protecting against HIV infection. (Updated  
 CC on 17-OCT-2003 to standardise OS field)

XX Sequence 36 AA;

Query Match 100.0%; Score 200; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36  
 |||||  
 Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36

## RESULT 4

AAB54787

ID AAB54787 standard; peptide; 36 AA.

XX  
 AC AAB54787;

DT 11-SEP-2003 (revised)  
 DT 05-MAR-2001 (first entry)

XX HIV antiviral activity exhibiting peptide SEQ ID NO:4.

XX Long lasting fusion peptide inhibitor; viral infection; antiviral;  
 KW antifusogenic; mobile blood component; measles virus; MeV; SIV;  
 KW simian immunodeficiency virus; human parainfluenza virus; HPiV; RSV;  
 KW human respiratory syncytial virus; human immunodeficiency virus; HIV.

OS Human immunodeficiency virus 1.  
 PN WO200069902-A1.  
 XX 23-NOV-2000.  
 XX 17-MAY-2000; 2000WO-US013651.  
 XX 17-MAY-1999; 99US-0134406P.  
 XX 10-SEP-1999; 99US-0153406P.  
 XX (CONJ-) CONJUCHEM INC.  
 XX Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;  
 PI WPI; 2001-007496/01.  
 XX A modified peptide and a reactive group which is reactive with amino  
 PT groups, hydroxyl groups, or thiol groups on blood components to form  
 PT stable covalent bonds useful for treatment of viral infections, e.g.  
 PT human immunodeficiency virus.  
 XX  
 PS Claim 6; Page 173-174; 21pp; English.  
 XX The present invention describes a modified anti-viral peptide (I)  
 CC comprising a peptide that exhibits anti-viral activity and a reactive  
 CC group which is reactive with amino groups, hydroxyl groups, or thiol  
 CC groups on blood components to form stable covalent bonds. (I) has anti-  
 CC viral and anti-fusogenic activities. (I) inhibits viral infection of  
 CC cells by inhibiting cell-cell fusion or free virus infection or to reduce  
 CC the level of membrane fusion events between two or more entities, e.g.,  
 CC virus-cell or cell-cell, relative to the level of membrane fusion that  
 CC occurs in the absence of the peptide. (I) is useful in the treatment of  
 CC patients who are suffering from viral infection, e.g. HIV, RSV, HPV, MeV,  
 CC and SIV. (I) may be administered prophylactically to previously  
 CC uninfected individuals. This is useful in cases where an individual has  
 CC been subjected to a high risk of exposure to a virus. By bonding of long-  
 CC lived components of the blood, such as immunoglobulin, serum albumin, red  
 CC blood cells and platelets the activity is extended for days to weeks.  
 CC This is due to improved stability in vivo and a reduced susceptibility to  
 CC peptidase or protease degradation. This minimises the need for more  
 CC frequent, or even continual, administration of the peptides. AAB54784 to  
 CC AAB5431 represent peptides used in the exemplification of the present  
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
 XX  
 SQ Sequence 36 AA;  
 Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKRWANLWNWF 36  
 DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKRWANLWNWF 36  
 RESULT 5  
 AAB92246  
 ID AAB92246 standard; peptide; 36 AA.  
 XX AAB92246;  
 XX 22-JUN-2001 (first entry)  
 XX Virus related peptide SEQ ID NO:1422.  
 XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KW blood component; modification; succinimidyl; maleimido group; amino;  
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX Homo sapiens.  
 OS Synthetic.

PN WO200069900-A2.  
 XX 23-NOV-2000.  
 XX 17-MAY-2000; 2000WO-US013576.  
 XX 17-MAY-1999; 99US-0134406P.  
 XX 10-SEP-1999; 99US-0153406P.  
 XX 15-OCT-1999; 99US-0159783P.  
 XX (CONJ-) CONJUCHEM INC.  
 XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
 PI WPI; 2001-112059/12.  
 XX  
 PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity.  
 XX  
 PS Disclosure; Page 662-663; 73pp; English.  
 XX The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity in  
 CC vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specificity as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 36 AA;  
 Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKRWANLWNWF 36  
 DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKRWANLWNWF 36  
 RESULT 6  
 AAB78239  
 ID AAB78239 standard; peptide; 36 AA.  
 XX AAB78239;  
 XX 19-APR-2001 (first entry)  
 XX Core polypeptide T1407.  
 XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;  
 KW antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;  
 KW fusion-related disorder; bacterial infection; viral infection.  
 XX Unidentified.  
 OS  
 XX WO200103723-A1.  
 XX 18-JAN-2001.  
 XX 10-JUL-2000; 2000WO-US018772.  
 XX 09-JUL-1999; 99US-00350641.

XX (TRIM-) TRIMERIS INC.  
 XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 PI WPI; 2001-147136/15.  
 XX  
 XX New hybrid polypeptide, useful for preventing, treating and diagnosing  
 PT e.g. viral infections, comprises an enhancer peptide linked to a core  
 PT polypeptide.  
 XX  
 XX Disclosure; Page 58; 15lpp; English.  
 XX  
 XX The present sequence is a core polypeptide which may be linked to an  
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of the  
 CC core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving coiled-  
 CC coil peptide interactions. Other uses include preventing, treating and/or  
 CC diagnosing disorders involving fusion events (e.g. modulation of  
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes  
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral  
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral  
 CC infections caused by human immunodeficiency virus, respiratory syncytial  
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and  
 CC polio virus). The enhancer peptide sequence increases the half-life and  
 CC reduces the clearance rate of therapeutic peptides, which increases their  
 CC efficacy and minimises the incidence and severity of adverse side  
 CC effects. In addition, this increases the sensitivity of the diagnostic  
 CC procedure in which they are used  
 XX  
 XX Sequence 36 AA;  
 SQ  
 Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36  
 DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36  
 RESULT 7  
 AAB78240  
 ID AAB78240 standard; peptide; 36 AA.  
 AC AAB78240;  
 DT 19-APR-2001 (first entry)  
 XX  
 DE Core polypeptide T1408.  
 XX  
 KW Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;  
 KW antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;  
 KW fusion-related disorder; bacterial infection; viral infection.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200103723-A1.  
 PD 18-JAN-2001.  
 XX  
 PF 10-JUL-2000; 2000WO-US018772.  
 XX  
 PR 09-JUL-1999; 99US-00350641.  
 XX  
 PA (TRIM-) TRIMERIS INC.  
 XX  
 PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX WPI; 2001-147136/15.  
 DR

XX New hybrid polypeptide, useful for preventing, treating and diagnosing  
 PT e.g. viral infections, comprises an enhancer peptide linked to a core  
 PT polypeptide.  
 XX  
 XX Disclosure; Page 58; 15lpp; English.  
 XX  
 XX The present sequence is a core polypeptide which may be linked to an  
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of the  
 CC core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving coiled-  
 CC coil peptide interactions. Other uses include preventing, treating and/or  
 CC diagnosing disorders involving fusion events (e.g. modulation of  
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes  
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral  
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral  
 CC infections caused by human immunodeficiency virus, respiratory syncytial  
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and  
 CC polio virus). The enhancer peptide sequence increases the half-life and  
 CC reduces the clearance rate of therapeutic peptides, which increases their  
 CC efficacy and minimises the incidence and severity of adverse side  
 CC effects. In addition, this increases the sensitivity of the diagnostic  
 CC procedure in which they are used  
 XX  
 XX Sequence 36 AA;  
 SQ  
 Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36  
 DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36  
 RESULT 8  
 AAU70181  
 ID AAU70181 standard; peptide; 36 AA.  
 XX  
 AC AAU70181;  
 XX  
 DT 14-FEB-2002 (first entry)  
 XX  
 DE HIV viral envelope protein stabilising peptide #3.  
 XX  
 KW Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;  
 KW anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;  
 KW alpha-helical region; ectodomain.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200170262-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PF 15-MAR-2001; 2001WO-US008108.  
 XX  
 PR 17-MAR-2000; 2000US-0189981P.  
 XX  
 PA (PANA-) PANACOS PHARM INC.  
 XX  
 PI Wild CT, Allaway GP;  
 XX  
 DR WPI; 2001-626098/72.  
 XX  
 PT Immunogenic composition for inhibiting HIV infection, comprises viral  
 PT envelope protein or its fragment exterior to viral membrane, a  
 PT stabilizing peptide, and, optionally, viral cell surface receptor or its  
 PT fragment.  
 XX



PS Claim 6; Page 45; 84pp; English.

CC The invention relates to methods of generating immunogens that elicit  
 CC neutralising antibodies which target regions of viral envelope proteins  
 CC such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-  
 CC 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and  
 CC AAU70677-AAU70743 represent stabilising peptides modelling the alpha-  
 CC helical regions of the ectodomain of the HIV-1 transmembrane protein to  
 CC stabilise fusion-active intermediate structures, which can be used as  
 CC vaccine immunogens. Immunogenic compositions comprise a viral envelope  
 CC protein or its fragment exterior to the viral membrane, a stabilising  
 CC peptide to disrupt formation of structural intermediates necessary for  
 CC viral fusion and entry, and optionally, a viral cell surface receptor or  
 CC its fragment. The stabilising peptide is capable of associating with the  
 CC envelope protein or its fragment to form a stabilised, fusion active  
 CC structure. Antibody binding assays are used to determine the ability of  
 CC immunogen vaccines to generate an immune response to various forms of  
 CC envelope. Virus neutralisation assays can be used to characterise the  
 CC antibody response raised against HIV-1 gp41 domains. The sequences and  
 CC methods are useful for inhibiting HIV infection, for inducing an immune  
 CC response in an animal and for raising antibodies

SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQKEQELLELDKQANLWNWF 36  
 |||||  
 DB 1 YTGIIYNLLEESQNOQKEQELLELDKQANLWNWF 36

RESULT 9

ABB02832  
 ID ABB02832 standard; peptide; 36 AA.

XX AC ABB02832;

XX 11-SEP-2003 (revised)  
 DT 06-AUG-2003 (revised)  
 DT 03-JAN-2002 (first entry)

XX Viral core polypeptide, SEQ ID NO: 1359.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.

XX Viruses.

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US003988.

XX 29-FEB-2000; 2000US-00515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection.

XX Disclosure; Page 525; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-

CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
 CC regions of proteins interact non-covalently with each other and/or with  
 CC peptides derived from them. This interaction is required for normal  
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
 CC peptide analogues may be used to inhibit respiratory syncytial virus  
 CC (RSV) infection in a cell. They may also be used to inhibit HIV  
 CC infection. The present sequence is a peptide provided in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
 CC 11-SEP-2003 to standardise OS field)

XX SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQKEQELLELDKQANLWNWF 36  
 |||||  
 DB 1 YTGIIYNLLEESQNOQKEQELLELDKQANLWNWF 36

RESULT 10

ABB02831  
 ID ABB02831 standard; peptide; 36 AA.

XX AC ABB02831;

XX 11-SEP-2003 (revised)  
 DT 06-AUG-2003 (revised)  
 DT 03-JAN-2002 (first entry)

XX Viral core polypeptide, SEQ ID NO: 1358.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.

XX Viruses.

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US003988.

XX 29-FEB-2000; 2000US-00515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;

XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection.

XX Disclosure; Page 524-525; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
 CC regions of proteins interact non-covalently with each other and/or with  
 CC peptides derived from them. This interaction is required for normal  
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
 CC peptide analogues may be used to inhibit respiratory syncytial virus  
 CC (RSV) infection in a cell. They may also be used to inhibit HIV  
 CC infection. The present sequence is a peptide provided in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
 CC 11-SEP-2003 to standardise OS field)

SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36  
 |||||  
 DB 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36  
 |||||

RESULT 11

AAG67041  
 ID AAG67041 standard; peptide; 36 AA.

AC AAG67041;  
 XX  
 DT 11-SEP-2003 (revised)  
 DT 03-JAN-2002 (first entry)  
 XX  
 DE HIV-1 gp41 peptide DP178 homologue DP-185.

KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection; DP185.

XX Human immunodeficiency virus 1.

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US003988.

XX 29-FEB-2000; 2000US-00515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection.

XX Example; Fig 1; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
 CC regions of proteins interact non-covalently with each other and/or with  
 CC peptides derived from them. This interaction is required for normal  
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
 CC peptide analogues may be used to inhibit respiratory syncytial virus  
 CC (RSV) infection in a cell. They may also be used to inhibit HIV  
 CC infection. The present sequence is a peptide provided in the  
 CC specification. (Updated on 11-SEP-2003 to standardise OS field)

SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36  
 |||||  
 DB 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36  
 |||||

RESULT 12

ABB01246

ID ABB01246 standard; peptide; 36 AA.

XX ABB01246;

XX 11-SEP-2003 (revised)

DT 06-AUG-2003 (revised)

DT 03-JAN-2002 (first entry)

XX Viral DP178/107-like region peptide T1407.

XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.

XX Viruses.

XX Key Location/Qualifiers

FT Modified-site 1

FT Modified-site 36 /note= "N-terminal is substituted by Ac"

FT Modified-site 36 /note= "C-terminal amide"

XX WO200164013-A2.

XX 07-SEP-2001.

XX 07-FEB-2001; 2001WO-US003988.

XX 29-FEB-2000; 2000US-00515965.

XX (TRIM-) TRIMERIS INC.

XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI; 2001-514829/56.

XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection.

XX Disclosure; Page 58; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
 CC regions of proteins interact non-covalently with each other and/or with  
 CC peptides derived from them. This interaction is required for normal  
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
 CC peptide analogues may be used to inhibit respiratory syncytial virus  
 CC (RSV) infection in a cell. They may also be used to inhibit HIV  
 CC infection. The present sequence is a peptide provided in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
 CC 11-SEP-2003 to standardise OS field)

SQ Sequence 36 AA;

Query Match 100.0%; Score 200; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36  
 |||||

DB 1 YTGIIYNLLSESONQOEKNEQELLELDKWANLWNWF 36  
 |||||

RESULT 13

ABB01247

ID ABB01247 standard; peptide; 36 AA.

XX ABB01247;

XX 11-SEP-2003 (revised)

DT	06-AUG-2003 (revised)	
DT	03-JAN-2002 (first entry)	
XX		
DE	Viral DP178/107-like region peptide T1408.	
XX		
DE	Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;	
KW	virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;	
KW	infection.	
XX		
OS	Viruses.	
XX		
XX	WO200164013-A2.	
PN		
XX		
PD	07-SEP-2001.	
XX		
XX	07-FEB-2001; 2001WO-US003988.	
PF		
XX		
PR	29-FEB-2000; 2000US-00515965.	
XX		
XX	(TRIM-) TRIMERIS INC.	
PA		
XX		
PI	Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;	
XX		
XX	WPI; 2001-514829/56.	
DR		
XX		
PT	Heptad repeat region peptide analogs useful for inhibiting virus/cells	
PT	fusion, useful for treating HIV and Respiratory Syncytial Virus	
PT	infection.	
XX		
PS	Disclosure; Page 58; 587pp; English.	
XX		
CC	The invention relates to isolated analogues of the heptad repeat region	
CC	peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-	
CC	673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)	
CC	respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2	
CC	regions of proteins interact non-covalently with each other and/or with	
CC	peptides derived from them. This interaction is required for normal	
CC	infectivity of viruses such as RSV and HIV. The heptad repeat region	
CC	peptide analogues may be used to inhibit respiratory syncytial virus	
CC	(RSV) infection in a cell. They may also be used to inhibit HIV	
CC	infection. The present sequence is a peptide provided in the	
CC	specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on	
CC	11-SEP-2003 to standardise OS field)	
XX		
SQ	Sequence 36 AA;	
	Query Match 100.0%; Score 200; DB 4; Length 36;	
	Best Local Similarity 100.0%; Pred. No. 1.4e-17;	
	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1 YTGIIYNLLEESQNQQEKNEQELLELDKQWNLWNWF 36	
Db	1 YTGIIYNLLEESQNQQEKNEQELLELDKQWNLWNWF 36	
RESULT 14		
AAU13793		
ID	AAU13793 standard; peptide; 36 AA.	
XX		
AC	AAU13793;	
XX		
DT	21-NOV-2001 (first entry)	
XX		
DE	DP178-like/DP107-like peptide T-1408.	
XX		
KW	Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;	
KW	antifusogenic; antiviral; HIV transmission; mutant; mutein.	
XX		
OS	Human immunodeficiency virus 1; isolate LAI.	
OS	Synthetic.	
XX		
PN	WO200151673-A2.	
XX		

PD	19-JUL-2001.	
XX		
XX	05-JUL-2000; 2000WO-US035727.	
XX		
PR	09-JUL-1999; 99US-00350841.	
XX		
PA	(TRIM-) TRIMERIS INC.	
XX		
XX	Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;	
PI	WPI; 2001-442157/47.	
XX		
DR		
XX		
FT	Identifying a compound that inhibits the formation of or disrupts a	
PT	DP107/DP178 complex, especially compounds with antitumorigenic, antiviral	
PT	or intracellular modulatory activity, by detecting the formation of a	
PT	DP107/DP178 complex.	
XX		
XX	Disclosure; Page 77; 259pp; English.	
PS		
XX		
CC	The present invention relates to peptides which exhibit anti-retroviral	
CC	activity. The peptides of the invention (AAU12559-AAU14009) comprise	
CC	DP178-like and DP107-like peptides. The DP178 peptide corresponds to	
CC	amino acids 639-673 of the transmembrane protein gp41 from human	
CC	immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide	
CC	corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention	
CC	also relates to a method of identifying compounds that inhibit the	
CC	formation of or disrupts a DP107/DP178 complex. The method comprises	
CC	detecting the formation of a DP107/DP178 complex, both in the presence or	
CC	absence of a test compound in a reaction mixture containing DP107 and	
CC	DP178 peptides. The method is useful for identifying compounds, including	
CC	small molecule compounds, which may themselves exhibit antitumorigenic,	
CC	antiviral or intracellular modulatory activity. The DP178-like/DP107-like	
CC	peptides are useful to inhibit human and non-human retroviral,	
CC	particularly HIV, transmission to uninfected cells. The present sequence	
CC	represents one of the DP178-like/DP107-like peptides of the invention	
XX		
SQ	Sequence 36 AA;	
	Query Match 100.0%; Score 200; DB 4; Length 36;	
	Best Local Similarity 100.0%; Pred. No. 1.4e-17;	
	Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 YTGIIYNLLEESQOQEKNEQELLELDKQANLWNWF 36	
Db	1 YTGIIYNLLEESQOQEKNEQELLELDKQANLWNWF 36	
RESULT 15		
AAU13792		
ID	AAU13792 standard; peptide; 36 AA.	
XX		
AC	AAU13792;	
XX		
DT	21-NOV-2001 (first entry)	
XX		
DE	DP178-like/DP107-like peptide T-1407.	
XX		
KW	Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;	
XX	antitumorigenic; antiviral; HIV transmission; mutant; mutein.	
OS	Human immunodeficiency virus 1; isolate LAI.	
OS	Synthetic.	
XX		
PH	Key Location/Qualifiers	
FT	Modified-site 1	
FT	/note= "N-terminal is substituted by Ac"	
FT	Modified-site 36	
FT	/note= "C-terminal amide"	
XX		
XX		
FN	W0200151673-A2.	
XX		
PD	19-JUL-2001.	
XX		

PF 05-JUL-2000; 2000WO-US035727.  
XX  
PR 09-JUL-1999; 99US-00350841.  
XX  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
XX WPI; 2001-442157/47.  
DR  
XX  
XX  
PT Identifying a compound that inhibits the formation of or disrupts a  
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
PT or intracellular modulatory activity, by detecting the formation of a  
PT DP107/DP178 complex.  
XX  
XX  
PS Disclosure; Page 77; 259pp; English.  
XX  
XX The present invention relates to peptides which exhibit anti-retroviral  
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to  
CC amino acids 639-673 of the transmembrane protein gp41 from human  
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
CC also relates to a method of identifying compounds that inhibit the  
CC formation of or disrupts a DP107/DP178 complex. The method comprises  
CC detecting the formation of a DP107/DP178 complex, both in the presence or  
CC absence of a test compound, in a reaction mixture containing DP107 and  
CC DP178 peptides. The method is useful for identifying compounds, including  
CC small molecule compounds, which may themselves exhibit antifusogenic,  
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like  
CC peptides are useful to inhibit human and non-human retroviral,  
CC particularly HIV, transmission to uninfected cells. The present sequence  
CC represents one of the DP178-like/DP107-like peptides of the invention  
XX  
SQ Sequence 36 AA;  
  
Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1.4e-17;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36  
|||  
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36  
|||  
  
Search completed: March 6, 2006, 15:37:20  
Job time : 115.667 secs





C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 03-Nov-1995

C:Accession: S56313  
R:Taylor, C.B.; Green, P.J.  
Plant Mol. Biol. 28, 27-38, 1995  
A:Title: Identification and characterization of genes with unstable transcripts (GUTS)  
A:Reference number: S56313; MUID:95306789; PMID:7787185  
A:Accession: S56313  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-44 <TAY>  
A:Cross-references: UNIPARC:UPI000017B0A6

Query Match 18.5%; Score 37; DB 2; Length 44;

Best Local Similarity 19.4%; Pred. No. 6e+02; Mismatches 17; Indels 0; Gaps 0;

QY 5 IYNLEESONQOEKNEQELLELDKMANLWNW 35  
DB 2 VKRIQEVKMQSNPSDDPMSPLENTPEW 32

## RESULT 9

S77793  
transketolase (EC 2.2.1.1) - Mycoplasma capricolum (fragment)  
N:Alternate names: protein MC315  
C:Species: Mycoplasma capricolum  
C:Date: 09-Oct-1997 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C:Accession: S77793  
R:Boek, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.; Mol. Microbiol. 16, 955-967, 1995  
A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiology  
A:Reference number: S77793; MUID:96059641; PMID:7476192  
A:Accession: S77793  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-40 <BOR>  
A:Cross-references: UNIPROT:Q49047; UNIPARC:UPI00000B7B19; EMBL:Z33230; NID:G514477; PID  
A:Experimental source: ATCC 27343  
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, July 1994  
C:Genetics:  
A:Genetic code: SGC3  
C:Superfamily: transketolase; thiamin pyrophosphate-binding domain homology  
C:Keywords: transferase

Query Match 18.2%; Score 36.5; DB 2; Length 40;

Best Local Similarity 34.5%; Pred. No. 6.2e+02; Mismatches 10; Conservative 2; Mismatches 10; Indels 7; Gaps 1;

QY 3 GIYNLEESONQOEKNEQELLELDKMAN 31  
DB 2 GIIVVLFNKMVFNPKNPE-----WPN 23

## RESULT 10

I46523  
troponin T 4f - rabbit (fragment)  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 14-Feb-1997 #sequence\_revision 14-Feb-1997 #text\_change 13-Aug-1999  
C:Accession: I46523  
R:Briggs, M.M.; Lin, J.J.; Schachat, F.H.  
J. Muscle Res. Cell. Motil. 8, 1-12, 1987  
A:Title: The extent of amino-terminal heterogeneity in rabbit fast skeletal muscle troponin  
A:Reference number: I46522; MUID:87251333; PMID:2439538  
A:Accession: I46523  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-32 <BRI>  
A:Cross-references: UNIPARC:UPI000016C510; EMBL:U04978; NID:G440816; PIDN:AAA16031.1; PI  
C:Superfamily: troponin T

Query Match 18.0%; Score 36; DB 2; Length 32;

Best Local Similarity 46.2%; Pred. No. 5.5e+02; Mismatches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 10 BESQNOQOEKNEOE 22  
DB 11 BEAQEEVHEEE 23

## RESULT 11

I66797  
troponin T 3f - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I66797  
R:Briggs, M.M.; Schachat, F.  
Dev. Biol. 158, 503-509, 1993  
A:Title: Origin of fetal troponin T: Developmentally regulated splicing of a new exon in  
A:Reference number: I66797; MUID:93345743; PMID:834466  
A:Accession: I66797  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-38 <RES>  
A:Cross-references: UNIPROT:Q62620; UNIPARC:UPI00000E7D00; EMBL:U04981; NID:G440822; PIDN  
C:Superfamily: troponin T

Query Match 18.0%; Score 36; DB 2; Length 38;

Best Local Similarity 41.2%; Pred. No. 6.7e+02; Mismatches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 6 YNLEESONQOEKNEOE 22  
DB 13 YEEEAQEEVHEEE 29

## RESULT 12

T48342  
hypothetical protein F15A17.240 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: T48342  
R:Bevan, M.; Terry, N.; Ardiles, W.; Buyschaert, C.; Dasseville, R.; De Clerck, R.; De  
eves, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z24491  
A>Status: preliminary  
A:Accession: T48342  
A:Molecule type: DNA  
A:Residues: 1-41 <BEV>  
A:Cross-references: UNIPROT:Q9LYW4; UNIPARC:UPI00000AA77A; EMBL:AL163002  
A:Experimental source: cultivar Columbia; BAC clone F15A17  
C:Genetics:  
A:Map position: 5  
A>Note: F15A17.240

Query Match 18.0%; Score 36; DB 2; Length 41;

Best Local Similarity 31.6%; Pred. No. 7.3e+02; Mismatches 6; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 4 IYNLEESONQOEKNEOE 22  
DB 19 ILETILGGTEEDNQOE 37

## RESULT 13

S74261  
troponin T3f, fast skeletal muscle - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 13-Mar-1997 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
C:Accession: S74261  
R:Briggs, M.M.; Mearns, M.; Schmidt, J.M.; Schachat, F.  
FEBS Lett. 350, 37-40, 1994  
A:Title: Identification of a fetal exon in the human fast Troponin T gene.  
A:Reference number: S48660; MUID:94341369; PMID:8062920  
A:Accession: S74261  
A:Molecule type: mRNA

A:Residues: 1-48 <BRI>  
A:Cross-references: UNIPROT:P45378; UNIPARC:UPI00000711F8; EMBL:UI4644; NID:G557029; PID  
C:Superfamily: troponin T  
C:Keywords: alternative splicing; phosphoprotein; skeletal muscle

Query Match 18.0%; Score 36; DB 2; Length 48;  
Best Local Similarity 41.2%; Pred. No. 8.7e+02;  
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 6 YNLEESNQKKEQE 22  
DB 13 YEEEAQEEVEEQEE 29

RESULT 14  
T06923  
high light-inducible protein homolog - Cyanophora paradoxa cyanelle  
C:Species: cyanelle Cyanophora paradoxa  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T06923  
R:Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.  
submitted to the EMBL Data Library, July 1995  
A:Description: Nucleotide sequence of the cyanelle genome from Cyanophora paradoxa.  
A:Reference number: Z15840  
A:Accession: T06923  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-49 <STI>  
A:Cross-references: UNIPROT:P48367; UNIPARC:UPI000013A441; EMBL:U30821; NID:G1016083; PID  
A:Experimental source: strain Pringsheim LB555  
C:Genetics:  
A:Gene: ycf17  
A:Genome: cyanelle  
C:Superfamily: high light-inducible protein ss12542  
C:Keywords: cyanelle

Query Match 18.0%; Score 36; DB 2; Length 49;  
Best Local Similarity 80.0%; Pred. No. 8.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 31 NLWNW 35  
DB 6 NIWNW 10

RESULT 15  
I77411  
renin-2 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Oct-2004  
C:Accession: I77411  
R:Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Gross, K.W.  
Mol. Cell. Biol. 4, 2321-2331, 1984  
A:Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analysis  
A:Reference number: I57576; MUID:85085936; PMID:6392850  
A:Accession: I77411  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: DNA  
A:Residues: 1-30 <RES>  
A:Cross-references: UNIPROT:P00796; UNIPARC:UPI000016C94B; GB:K02801; NID:G200695; PIDN:  
C:Superfamily: Peptin

Query Match 17.5%; Score 35; DB 2; Length 30;  
Best Local Similarity 71.4%; Pred. No. 6.8e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 29 WANLWNW 35  
DB 9 WALLWLW 15

Search completed: March 6, 2006, 15:44:16  
Job time : 19.3333 secs







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Matches 31; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 YTGIIYNLLEESQOQKNEQELLELDKWANLWNWF 36
   |||||:|||||:|||||:|||||:|||||
Db 7 YTSLIYTLLEESQOQKNEQELLELDKWASLWNWF 42
   |||||:|||||:|||||:|||||:|||||

RESULT 6
Q69895_9HIV1
ID Q69895_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69895;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06725; AA19139.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6168 MW; 8077C4815B83281E CRC64;

Query Match 89.0%; Score 178; DB 2; Length 49;
Best Local Similarity 88.9%; Pred. No. 2.3e-13;
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 YTGIIYNLLEESQOQKNEQELLELDKWANLWNWF 36
   |||||:|||||:|||||:|||||:|||||
Db 14 YTGIIYTLLEESQOQKNEQELLELDKWASLWNWF 49
   |||||:|||||:|||||:|||||:|||||

RESULT 7
Q69896_9HIV1
ID Q69896_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69896;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06726; AA19139.1; -; mRNA.
DR HSSP; P31872; 1LB0.

Query Match 89.0%; Score 178; DB 2; Length 49;
Best Local Similarity 88.9%; Pred. No. 2.3e-13;
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 YTGIIYNLLEESQOQKNEQELLELDKWANLWNWF 36
   |||||:|||||:|||||:|||||:|||||
Db 14 YTGIIYTLLEESQOQKNEQELLELDKWASLWNWF 49
   |||||:|||||:|||||:|||||:|||||

RESULT 8
Q69908_9HIV1
ID Q69908_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69908;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06738; AA19151.1; -; mRNA.
DR HSSP; Q87973; 2SIV.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6283 MW; 74CD75339B92C172 CRC64;

Query Match 88.0%; Score 176; DB 2; Length 49;
Best Local Similarity 86.1%; Pred. No. 4e-13;
Matches 31; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 YTGIIYNLLEESQOQKNEQELLELDKWANLWNWF 36
   |||||:|||||:|||||:|||||:|||||
Db 14 YTSIIYTLLEESQOQKNEQELLELDKWTLNWNWF 49
   |||||:|||||:|||||:|||||:|||||

RESULT 9
Q69907_9HIV1
ID Q69907_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69907;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
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DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6167 MW; 0277C4815B8D26FE CRC64;

Query Match 89.0%; Score 178; DB 2; Length 49;
Best Local Similarity 88.9%; Pred. No. 2.3e-13;
Matches 32; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 YTGIIYNLLEESQOQKNEQELLELDKWANLWNWF 36
   |||||:|||||:|||||:|||||:|||||
Db 14 YTGIIYTLLEESQOQKNEQELLELDKWASLWNWF 49
   |||||:|||||:|||||:|||||:|||||

RESULT 8
Q69908_9HIV1
ID Q69908_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69908;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06738; AA19151.1; -; mRNA.
DR HSSP; Q87973; 2SIV.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6283 MW; 74CD75339B92C172 CRC64;

Query Match 88.0%; Score 176; DB 2; Length 49;
Best Local Similarity 86.1%; Pred. No. 4e-13;
Matches 31; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 YTGIIYNLLEESQOQKNEQELLELDKWANLWNWF 36
   |||||:|||||:|||||:|||||:|||||
Db 14 YTSIIYTLLEESQOQKNEQELLELDKWTLNWNWF 49
   |||||:|||||:|||||:|||||:|||||

RESULT 9
Q69907_9HIV1
ID Q69907_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69907;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
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RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06737; AAA19150.1; -; mRNA.
DR HSSP; O87973; 2SIV.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
FT NON_TER 49
SQ SEQUENCE 49 AA; 6241 MW; 29C4E5A8CBC7CDD8 CRC64;

Query Match 87.0%; Score 174; DB 2; Length 49;
Best Local Similarity 83.3%; Pred. No. 6.9e-13;
Matches 30; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQKQEKNEQELLELDKWNLNWNF 36
|||:|||||:|||||:|||||:|||||:|||||
Db 14 YTSLYTLLEESQTKQEKNEKELLELDKWNLNWNF 49

RESULT 10
Q69905_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69905;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06735; AAA19148.1; -; mRNA.
DR HSSP; F31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 34
FT NON_TER 34
SQ SEQUENCE 34 AA; 4196 MW; 7B724A8EA16ABD9C CRC64;

Query Match 85.5%; Score 171; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 1e-12;
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GIIVNLEESQKQEKNEQELLELDKWNLNWNF 36
|||:|||||:|||||:|||||:|||||:|||||
Db 1 GLIYTLLEKSQKQEKNEQELLELDKWNLNWNF 34

RESULT 11
Q69906_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69906;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06721; AAA19134.1; -; mRNA.
DR HSSP; F31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 41
FT NON_TER 41
SQ SEQUENCE 41 AA; 5082 MW; 0B9C7E2CDD403CC6 CRC64;

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ID Q69906_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69906;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06736; AAA19149.1; -; mRNA.
DR HSSP; F31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
FT NON_TER 49
SQ SEQUENCE 49 AA; 6214 MW; 29C4E5A8CBD63DD8 CRC64;

Query Match 84.5%; Score 169; DB 2; Length 49;
Best Local Similarity 80.6%; Pred. No. 2.6e-12;
Matches 29; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQKQEKNEQELLELDKWNLNWNF 36
|||:|||||:|||||:|||||:|||||:|||||
Db 14 YTSLYTLLEESQTKQEKNEKELLELDKWNLNWNF 49

RESULT 12
Q69891_9HIV1 PRELIMINARY; PRT; 41 AA.
AC Q69891;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06721; AAA19134.1; -; mRNA.
DR HSSP; F31872; ILB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 41
FT NON_TER 41
SQ SEQUENCE 41 AA; 5082 MW; 0B9C7E2CDD403CC6 CRC64;

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Query Match      84.0%; Score 168; DB 2; Length 41;
Best Local Similarity 88.2%; Pred. No. 2.8e-12;
Matches 30; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GIIYNLLEESQNOQKNEQELLELDKWANLWNWF 36
   |||||:|||||:|||||:|||||:|||||:|||||
Db 1 GIIYNLIETSQNOQKNEQELLELDKWASLWNWF 34

RESULT 13
Q69893_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69893;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OC NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06723; AAA19136.1; -; mRNA.
DR HSSP; P31872; ILB0.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1
FT NON TER 34
SQ SEQUENCE 34 AA; 4196 MW; 0C7CAA60A164B89C CRC64;

Query Match      83.0%; Score 166; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 3.9e-12;
Matches 30; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GIIYNLLEESQNOQKNEQELLELDKWANLWNWF 36
   |||||:|||||:|||||:|||||:|||||:|||||
Db 1 GLIYTLLEESQVQOQKNEQELLELDKWASLWNWF 34

RESULT 14
Q69894_9HIV1 PRELIMINARY; PRT; 34 AA.
AC Q69894;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OC NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
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DR EMBL; U06724; AAA19137.1; -; mRNA.
DR HSSP; P31872; ILB0.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1
FT NON TER 34
SQ SEQUENCE 34 AA; 4182 MW; A37CAA60A164AEF0 CRC64;

Query Match      83.0%; Score 166; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 3.9e-12;
Matches 30; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GIIYNLLEESQNOQKNEQELLELDKWANLWNWF 36
   |||||:|||||:|||||:|||||:|||||:|||||
Db 1 GLIYTLLEESQVQOQKNEQELLELDKWASLWNWF 34

RESULT 15
Q69892_9HIV1 PRELIMINARY; PRT; 41 AA.
AC Q69892;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OC NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06722; AAA19135.1; -; mRNA.
DR HSSP; P31872; ILB0.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1
FT NON TER 41
SQ SEQUENCE 41 AA; 5081 MW; 0B9C70CC33403CC6 CRC64;

Query Match      82.0%; Score 164; DB 2; Length 41;
Best Local Similarity 85.3%; Pred. No. 8.3e-12;
Matches 29; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GIIYNLLEESQNOQKNEQELLELDKWANLWNWF 36
   |||||:|||||:|||||:|||||:|||||:|||||
Db 1 GIIYNLIETSQNOQKNEQELLELDKWASLWNWF 34

Search completed: March 6, 2006, 15:43:15
Job time : 117.667 secs
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GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:43:35 ; Search time 27.6667 Seconds  
(without alignments)  
107.578 Million cell updates/sec

Title: US-09-809-060A-3

Perfect score: 200

Sequence: 1 YTGIIYNLEESQKQKNEQELLELDKQANLWVNF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfilese1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200	100.0	36	1 US-08-073-028-4	Sequence 4, Appli
2	200	100.0	36	2 US-08-486-099-4	Sequence 4, Appli
3	200	100.0	36	2 US-08-360-107A-4	Sequence 4, Appli
4	200	100.0	36	2 US-08-484-223B-4	Sequence 4, Appli
5	200	100.0	36	2 US-08-919-597-4	Sequence 4, Appli
6	200	100.0	36	2 US-08-475-668A-4	Sequence 4, Appli
7	200	100.0	36	2 US-08-485-551A-4	Sequence 4, Appli
8	200	100.0	36	2 US-08-471-913A-4	Sequence 4, Appli
9	200	100.0	36	2 US-08-554-616-4	Sequence 4, Appli
10	200	100.0	36	2 US-08-485-264A-4	Sequence 4, Appli
11	200	100.0	36	2 US-09-082-279B-1358	Sequence 1358, Ap
12	200	100.0	36	2 US-09-082-279B-1359	Sequence 1359, Ap
13	200	100.0	36	2 US-08-474-349A-4	Sequence 4, Appli
14	200	100.0	36	2 US-09-315-304B-1358	Sequence 1358, Ap
15	200	100.0	36	2 US-09-315-304B-1359	Sequence 1359, Ap
16	200	100.0	36	2 US-08-255-208A-4	Sequence 4, Appli
17	200	100.0	36	2 US-08-973-952-4	Sequence 4, Appli
18	200	100.0	36	2 US-08-470-896-4	Sequence 4, Appli
19	200	100.0	36	2 US-08-485-546A-4	Sequence 4, Appli
20	200	100.0	36	2 US-09-834-784-1358	Sequence 1358, Ap
21	200	100.0	36	2 US-09-834-784-1359	Sequence 1359, Ap
22	200	100.0	36	2 US-09-515-965A-1358	Sequence 1358, Ap
23	200	100.0	36	2 US-09-515-965A-1359	Sequence 1359, Ap
24	200	100.0	36	2 US-09-350-641C-1358	Sequence 1358, Ap
25	200	100.0	36	2 US-09-350-641C-1359	Sequence 1359, Ap
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27	200	100.0	36	2 US-09-350-841A-1359	Sequence 1359, Ap

28 200 100.0 36 2 US-08-487-266A-4 Sequence 4, Appli  
29 200 100.0 36 2 US-09-623-548A-1422 Sequence 1422, Ap  
30 200 100.0 36 2 US-10-252-138-4 Sequence 4, Appli  
31 200 100.0 36 2 US-09-657-276-1422 Sequence 1422, Ap  
32 200 100.0 36 2 US-08-484-741-4 Sequence 4, Appli  
33 184 92.0 36 1 US-08-073-028-3 Sequence 3, Appli  
34 184 92.0 36 2 US-08-360-107A-3 Sequence 3, Appli  
35 184 92.0 36 2 US-08-554-616-3 Sequence 1543, Ap  
36 184 92.0 36 2 US-09-350-841A-1543 Sequence 110, App  
37 182 91.0 46 2 US-08-965-056-110 Sequence 642, App  
38 180 90.0 36 2 US-09-082-279B-642 Sequence 642, App  
39 180 90.0 36 2 US-09-315-304B-642 Sequence 642, App  
40 180 90.0 36 2 US-09-834-784-642 Sequence 642, App  
41 180 90.0 36 2 US-09-515-965A-642 Sequence 642, App  
42 180 90.0 36 2 US-09-350-641C-642 Sequence 642, App  
43 180 90.0 36 2 US-09-350-841A-642 Sequence 642, App  
44 178 89.0 36 2 US-08-486-099-3 Sequence 3, Appli  
45 178 89.0 36 2 US-08-484-223B-3 Sequence 3, Appli

## ALIGNMENTS

## RESULT 1

US-08-073-028-4  
; Sequence 4, Application US/08073028  
; Patent No. 5464933  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,028  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-073-028-4

Query Match 100.0%; Score 200; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQKQKNEQELLELDKQANLWVNF 36  
|||||

Db 1 YTGIIYNLLEESQKNEQKQELLELDKWANLWNWF 36

## RESULT 2

US-08-486-099-4  
; Sequence 4, Application US/08486099  
; Patent No. 6013263  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,099  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-031  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-486-099-4

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 YTGIIYNLLEESQKNEQKQELLELDKWANLWNWF 36  
|||||  
Db 1 YTGIIYNLLEESQKNEQKQELLELDKWANLWNWF 36  
|||||  
RESULT 3  
US-08-360-107A-4  
; Sequence 4, Application US/08360107A  
; Patent No. 6017536  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,099  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-031  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-486-099-4

Query Match 100.0%; Score 200; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQKNEQKQELLELDKWANLWNWF 36

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Db 1 YTGIIYNLLEESQKNEQKQELLELDKWANLWNWF 36

## RESULT 3

US-08-360-107A-4  
; Sequence 4, Application US/08360107A  
; Patent No. 6017536  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
; NUMBER OF SEQUENCES: 245  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 149  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/360,107A  
; FILING DATE: 20-DEC-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-013  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-360-107A-4

Query Match 100.0%; Score 200; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQKNEQKQELLELDKWANLWNWF 36

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Db 1 YTGIIYNLLEESQKNEQKQELLELDKWANLWNWF 36

## RESULT 4

US-08-484-223B-4  
; Sequence 4, Application US/08484223B  
; Patent No. 6020459  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
; NUMBER OF SEQUENCES: 245  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS



SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/484,223B  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-4

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36  
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DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36

## RESULT 5

US-08-919-597-4  
Sequence 4, Application US/08919597  
Patent No. 6054265

## GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-4

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36  
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DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36

## RESULT 6

US-08-475-668A-4  
Sequence 4, Application US/08475668A  
Patent No. 6060065

## GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-4

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36  
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DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36

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RESULT 7
US-08-485-551A-4
; Sequence 4, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-485-551A-4

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNMF 36
| | | | | | | | | | | | | | | | | | | |
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNMF 36
| | | | | | | | | | | | | | | | | | | |

RESULT 8
US-08-471-913A-4
; Sequence 4, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
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; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-471-913A-4

Query Match 100.0%; Score 200; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 4.6e-18;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNMF 36
| | | | | | | | | | | | | | | | | | | |
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNMF 36
| | | | | | | | | | | | | | | | | | | |

RESULT 9
US-08-554-616-4
; Sequence 4, Application US/08554616
; Patent No. 6133418
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,616
; FILING DATE: 06-NOV-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/073,028
; FILING DATE: 07-JUN-1993
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ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-554-616-4

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36  
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 10  
US-08-485-264A-4  
Sequence 4, Application US/08485264A  
Patent No. 6228983  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 232  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/485,264A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide

US-08-485-264A-4

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36  
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 11  
US-09-082-279B-1358  
Sequence 1358, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohmed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1358  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-1358

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36  
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 12  
US-09-082-279B-1359  
Sequence 1359, Application US/09082279B  
Patent No. 6258782  
GENERAL INFORMATION:  
APPLICANT: Barney, Shawn  
APPLICANT: Guthrie, Kelly  
APPLICANT: Merutka, Gene  
APPLICANT: Anwer, Mohmed  
APPLICANT: Lambert, Dennis  
TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
FILE REFERENCE: 7872-043  
CURRENT APPLICATION NUMBER: US/09/082,279B  
CURRENT FILING DATE: 1998-05-20  
NUMBER OF SEQ ID NOS: 1515  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 1359  
LENGTH: 36  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Core polypeptide  
US-09-082-279B-1359

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNF 36  
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNF 36

## RESULT 13

US-08-474-349A-4  
; Sequence 4, Application US/08474349A  
; Patent No. 6333395  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA  
; TITLE OF INVENTION: VIRUS TRANSMISSION  
; NUMBER OF SEQUENCES: 517  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,349A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-474-349A-4

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNF 36  
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNF 36

## RESULT 14

US-09-315-304B-1358  
; Sequence 1358, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S. K.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merytka, G.  
; APPLICANT: Anwer, M.

; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1358  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
; US-09-315-304B-1358

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNF 36  
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNF 36

## RESULT 15

US-09-315-304B-1359  
; Sequence 1359, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S. K.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merytka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1359  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
; US-09-315-304B-1359

Query Match 100.0%; Score 200; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.6e-18;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNF 36  
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWLNWNF 36

Search completed: March 6, 2006, 15:45:44  
Job time : 27.6667 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:44:30 ; Search time 94 Seconds  
(without alignments)  
160.020 Million cell updates/sec

Title: US-09-809-060A-3

Perfect score: 200

Sequence: 1 YTGIIYNLLEESQKNEQKELLEDKQWLNWVF 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 549595

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:\*  
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2: /cgn2\_6/prodata1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/prodata1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/prodata1/pubpaa/US10A\_PUBCOMB.pep:\*  
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6: /cgn2\_6/prodata1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	200	100.0	36	3	US-09-809-060-3
2	200	100.0	36	4	US-10-252-136-4
3	200	100.0	36	4	US-10-351-641-1358
4	200	100.0	36	4	US-10-351-641-1359
5	200	100.0	36	4	US-10-267-682-4
6	200	100.0	36	4	US-10-267-748-4
7	200	100.0	36	4	US-10-663-589-39
8	200	100.0	36	4	US-10-671-282-39
9	200	100.0	36	5	US-10-168-295-4
10	200	100.0	36	5	US-10-950-010-4
11	200	100.0	36	6	US-11-066-697-1422
12	182	91.0	46	3	US-09-854-816-110
13	181	90.5	36	5	US-10-950-010-534
14	180	90.0	36	4	US-10-351-641-642
15	180	90.0	36	4	US-10-457-780-52
16	180	90.0	36	5	US-10-950-010-537
17	180	90.0	36	5	US-10-950-010-539
18	178	89.0	36	3	US-09-809-060-2
19	178	89.0	36	4	US-10-252-136-3
20	178	89.0	36	4	US-10-351-641-1357
21	178	89.0	36	4	US-10-267-682-3
22	178	89.0	36	4	US-10-267-748-3
23	178	89.0	36	4	US-10-663-589-38
24	178	89.0	36	4	US-10-671-282-38
25	178	89.0	36	5	US-10-168-295-3
26	178	89.0	36	5	US-10-950-010-3
27	178	89.0	36	6	US-11-066-697-1421

28	178	89.0	46	3	US-09-854-816-109	Sequence 109, App
29	177	88.5	36	4	US-10-351-641-856	Sequence 856, App
30	177	88.5	36	5	US-10-950-010-536	Sequence 536, App
31	177	88.5	36	5	US-10-950-010-541	Sequence 541, App
32	176	88.0	36	3	US-09-809-060-19	Sequence 19, Appl
33	176	88.0	36	3	US-09-779-451-44	Sequence 44, Appl
34	176	88.0	36	4	US-10-351-641-1051	Sequence 1051, Ap
35	176	88.0	36	4	US-10-685-801-44	Sequence 44, Appl
36	176	88.0	36	4	US-10-660-206-44	Sequence 17, Appl
37	176	88.0	46	3	US-09-809-060-17	Sequence 42, Appl
38	176	88.0	46	3	US-09-779-451-42	Sequence 42, Appl
39	176	88.0	46	4	US-10-685-801-42	Sequence 42, Appl
40	176	88.0	46	4	US-10-660-206-42	Sequence 42, Appl
41	175	87.5	36	3	US-09-809-060-1	Sequence 1, Appl
42	175	87.5	36	3	US-09-809-060-85	Sequence 85, Appl
43	175	87.5	36	3	US-09-796-202-10	Sequence 10, Appl
44	175	87.5	36	3	US-09-960-717-2	Sequence 2, Appl
45	175	87.5	36	3	US-09-779-451-5	Sequence 5, Appl

#### ALIGNMENTS

##### RESULT 1

US-09-809-060-3  
; Sequence 3, Application US/09809060  
; Publication No. US20020010317A1  
; GENERAL INFORMATION:  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Allaway, Graham P.  
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit  
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active  
; TITLE OF INVENTION: Regions of HIV Envelope Proteins  
; FILE REFERENCE: 1900.0260001  
; CURRENT APPLICATION NUMBER: US/09/809,060  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: US 60/189,981  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-809-060-3

Query Match	100.0%	Score 200;	DB 3;	Length 36;
Best Local Similarity	100.0%	Pred. No. 2.6e-16;		
Matches	36;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	YTGIIYNLLEESQKNEQKELLEDKQWLNWVF	36	
DB	1	YTGIIYNLLEESQKNEQKELLEDKQWLNWVF	36	

##### RESULT 2

US-10-252-136-4  
; Sequence 4, Application US/10252136  
; Publication No. US20030103998A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, M. Ross  
; APPLICANT: Lambert, Dennis M.  
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER  
; TITLE OF INVENTION: VIRAL INFECTIONS  
; TITLE OF INVENTION: USING COMBINATORY THERAPY  
; FILE REFERENCE: 7872-036  
; CURRENT APPLICATION NUMBER: US/10/252,136  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: US/08/973,952  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4

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; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-4

Query Match      100.0%; Score 200; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 3
US-10-351-641-1358
; Sequence 1358, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1358
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1358

Query Match      100.0%; Score 200; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 4
US-10-351-641-1359
; Sequence 1359, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
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; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1359
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1359

Query Match      100.0%; Score 200; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.6e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 5
US-10-267-682-4
; Sequence 4, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELETYPE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-267-682-4
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Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36  
DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 6  
US-10-267-748-4  
; Sequence 4, Application US/10267748  
; Publication No. US20040052820A1  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; Addresser: Pennie & Edmonds  
; Wild, Carl T.  
; Barney, Shawn O.  
; Lambert, Dennis M.  
; Petteway, Stephen R.  
; Langlois, Alphonse J.  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION  
; NUMBER OF SEQUENCES: 239  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/10/267,748  
; FILING DATE: 08-Oct-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION NUMBER: US/08/484,223A  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-029  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-267-748-4

Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36  
DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 7

US-10-663-589-39  
; Sequence 39, Application US/10663589  
; Publication No. US20040063637A1  
; GENERAL INFORMATION:  
; APPLICANT: Trimeris, Inc.  
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV  
; FILE REFERENCE: TRM-003  
; CURRENT APPLICATION NUMBER: US/10/663,589  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: US 60/414,441  
; PRIOR FILING DATE: 2002-09-27  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 39  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthesized  
US-10-663-589-39

Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36  
DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 8

US-10-671-282-39  
; Sequence 39, Application US/10671282  
; Publication No. US20040122214A1  
; GENERAL INFORMATION:  
; APPLICANT: Trimeris, Inc.  
; TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and  
; FILE REFERENCE: TRM-004  
; CURRENT APPLICATION NUMBER: US/10/671,282  
; CURRENT FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: 60/414,439  
; PRIOR FILING DATE: 2002-09-27  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 39  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthesized  
US-10-671-282-39

Query Match 100.0%; Score 200; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.6e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36  
DB 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 9

US-10-168-295-4  
; Sequence 4, Application US/10168295  
; Publication No. US20050065319A1  
; GENERAL INFORMATION:  
; APPLICANT: Baroudy, Bahige M.  
; TITLE OF INVENTION: Combination Method For Treating Viral Infections  
; FILE REFERENCE: IN01358  
; CURRENT APPLICATION NUMBER: US/10/168,295  
; CURRENT FILING DATE: 2002-06-19

APPLICANT: Milner, Peter G.  
APPLICANT: Holmes, Darren L.

APPLICANT: Milner, Peter G.  
APPLICANT: Holmes, Darren L.

TELEFAX: 650/952-9

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: P1005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881





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;/ PRIOR APPLICATION NUMBER: 60/539,207  
;/ PRIOR FILING DATE: 2004-01-26  
;/ PRIOR APPLICATION NUMBER: 60/487,964  
;/ PRIOR FILING DATE: 2003-07-17  
;/ PRIOR APPLICATION NUMBER: 60/469,600  
;/ PRIOR FILING DATE: 2003-05-06  
;/ NUMBER OF SEQ ID NOS: 91  
;/ SOFTWARE: PatentIn Ver. 3.2  
;/ SEQ ID NO 1  
;/ LENGTH: 36  
;/ TYPE: PRT  
;/ ORGANISM: Human immunodeficiency virus  
US-11-029-003-1

Query Match 87.5%; Score 175; DB 7; Length 36;  
Best Local Similarity 83.3%; Pred. No. 1.6e-15;  
Matches 30; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36  
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Db 1 YTSLIHSLIEESQKQKNEQELLELDKQWLNWNWF 36

## RESULT 3

US-11-187-687-22  
;/ Sequence 22, Application US/11187687  
;/ Publication No. US20060019347A1  
;/ GENERAL INFORMATION:

;/ APPLICANT: Cho, Ho Sung  
;/ APPLICANT: Daniel, Thomas O.  
;/ APPLICANT: Hays, Anna-Maria  
;/ APPLICANT: Wilson, Troy E.  
;/ APPLICANT: Litzinger, David C.  
;/ APPLICANT: Mariani, Roberto  
;/ APPLICANT: Kimmel, Bruce E.  
;/ APPLICANT: Keefe, William M.  
;/ TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino  
;/ FILE OF INVENTION: Acids  
;/ FILE REFERENCE: AMBX-0041.00US  
;/ CURRENT APPLICATION NUMBER: US/11/187,687  
;/ CURRENT FILING DATE: 2005-07-21  
;/ PRIOR APPLICATION NUMBER: 60/590,035  
;/ PRIOR FILING DATE: 2004-07-21  
;/ PRIOR APPLICATION NUMBER: 60/659,709  
;/ PRIOR FILING DATE: 2005-03-07  
;/ NUMBER OF SEQ ID NOS: 28  
;/ SOFTWARE: PatentIn version 3.3  
;/ SEQ ID NO 22  
;/ LENGTH: 36  
;/ TYPE: PRT  
;/ ORGANISM: Human immunodeficiency virus

US-11-187-687-22

Query Match 87.5%; Score 175; DB 7; Length 36;  
Best Local Similarity 83.3%; Pred. No. 1.6e-15;  
Matches 30; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36  
|| :||:|||||  
Db 1 YTSLIHSLIEESQKQKNEQELLELDKQWLNWNWF 36

## RESULT 4

US-11-112-277-33  
;/ Sequence 33, Application US/11112277  
;/ Publication No. US20050267293A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Bousquet-Gagnon, Nathalie  
;/ APPLICANT: Quraishi, Omar  
;/ APPLICANT: Bridon, Dominique P.  
;/ TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN  
;/ FILE OF INVENTION: CONJUGATES  
;/ FILE REFERENCE: 500862003700

;/ CURRENT APPLICATION NUMBER: US/11/112,277  
;/ CURRENT FILING DATE: 2005-04-22  
;/ PRIOR APPLICATION NUMBER: US 60/565,228  
;/ PRIOR FILING DATE: 2004-04-23  
;/ NUMBER OF SEQ ID NOS: 53  
;/ SOFTWARE: FastSeq for Windows Version 4.0  
;/ SEQ ID NO 33  
;/ LENGTH: 37  
;/ TYPE: PRT  
;/ ORGANISM: Artificial Sequence  
;/ FEATURE:  
;/ OTHER INFORMATION: T20 Analogue  
;/ FEATURE:  
;/ NAME/KEY: MOD\_RES  
;/ LOCATION: 37  
;/ OTHER INFORMATION: Xaa is Lys linked to ABEA-MPA  
US-11-112-277-33

Query Match 87.5%; Score 175; DB 7; Length 37;  
Best Local Similarity 83.3%; Pred. No. 1.7e-15;  
Matches 30; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36  
|| :||:|||||  
Db 1 YTSLIHSLIEESQKQKNEQELLELDKQWLNWNWF 36

## RESULT 5

US-11-187-687-24  
;/ Sequence 24, Application US/11187687  
;/ Publication No. US20060019347A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Cho, Ho Sung  
;/ APPLICANT: Daniel, Thomas O.  
;/ APPLICANT: Hays, Anna-Maria  
;/ APPLICANT: Wilson, Troy E.  
;/ APPLICANT: Litzinger, David C.  
;/ APPLICANT: Mariani, Roberto  
;/ APPLICANT: Kimmel, Bruce E.  
;/ APPLICANT: Keefe, William M.  
;/ TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino  
;/ FILE OF INVENTION: Acids  
;/ FILE REFERENCE: AMBX-0041.00US  
;/ CURRENT APPLICATION NUMBER: US/11/187,687  
;/ CURRENT FILING DATE: 2005-07-21  
;/ PRIOR APPLICATION NUMBER: 60/590,035  
;/ PRIOR FILING DATE: 2004-07-21  
;/ PRIOR APPLICATION NUMBER: 60/659,709  
;/ PRIOR FILING DATE: 2005-03-07  
;/ NUMBER OF SEQ ID NOS: 28  
;/ SOFTWARE: PatentIn version 3.3  
;/ SEQ ID NO 24  
;/ LENGTH: 44  
;/ TYPE: PRT  
;/ ORGANISM: Human immunodeficiency virus  
US-11-187-687-24

Query Match 87.5%; Score 175; DB 7; Length 44;  
Best Local Similarity 83.3%; Pred. No. 2e-15;  
Matches 30; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWLNWNWF 36  
|| :||:|||||  
Db 9 YTSLIHSLIEESQKQKNEQELLELDKQWLNWNWF 44

## RESULT 6

US-11-089-426-10  
;/ Sequence 10, Application US/11089426  
;/ Publication No. US20050261229A1  
;/ GENERAL INFORMATION:  
;/ APPLICANT: Gillies, Stephen D.  
;/ APPLICANT: Lo, Kin-Ming

RESULT 8  
US-10-506-796A-5  
; Sequence 5, Application US/10506796A  
; Publication No. US20060013831A1  
; GENERAL INFORMATION:  
; APPLICANT: MOR. Tsafir

RESULT 10  
US-10-506-796A-1  
; Sequence 1; Application US/10506796A  
; Publication No. US20060013831A1  
; GENERAL INFORMATION:

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; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(35)
; OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
US-10-506-796A-1

Query Match      66.0%; Score 132; DB 6; Length 35;
Best Local Similarity 92.0%; Pred. No. 3.2e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 SQOQEKNEQELLELDKWANLWNWF 36
Db 1 SQTQEKNEQELLELDKWASLWNWF 25

RESULT 11
US-10-506-796A-3
; Sequence 3, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-506-796A-3

Query Match      66.0%; Score 132; DB 6; Length 36;
Best Local Similarity 92.0%; Pred. No. 3.3e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 SQOQEKNEQELLELDKWANLWNWF 36
Db 2 SQTQEKNEQELLELDKWASLWNWF 26

RESULT 12
US-10-506-796A-4
; Sequence 4, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
```

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; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(35)
; OTHER INFORMATION: HIV-1 isolate MN clone v5 (residues 649-685)
US-10-506-796A-4

Query Match      60.0%; Score 120; DB 6; Length 36;
Best Local Similarity 84.0%; Pred. No. 9.8e-09;
Matches 21; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 SQOQEKNEQELLELDKWANLWNWF 36
Db 1 SQTQEKNEQELLELDKWESLWNWF 25

RESULT 13
US-10-841-956A-3
; Sequence 3, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-3

Query Match      59.5%; Score 119; DB 6; Length 39;
Best Local Similarity 72.4%; Pred. No. 1.4e-08;
Matches 21; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 8 LLEBSQOQEKNEQELLELDKWANLWNWF 36
Db 11 LLEQAQIQOQEKNEYELQKLDKWASLWNWF 39

RESULT 14
US-11-029-003-3
; Sequence 3, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEL, JAMES
```

## ; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS

; FILE REFERENCE: 08945.0007-01000  
; CURRENT APPLICATION NUMBER: US/11/029,003  
; CURRENT FILING DATE: 2005-01-05  
; PRIOR APPLICATION NUMBER: 60/539,207  
; PRIOR FILING DATE: 2004-01-26  
; PRIOR APPLICATION NUMBER: 60/487,964  
; PRIOR FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: 60/469,600  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 3  
; LENGTH: 39  
; TYPE: PRT

; ORGANISM: Human immunodeficiency virus  
US-11-029-003-3

Query Match 59.5%; Score 119; DB 7; Length 39;  
Best Local Similarity 72.4%; Pred. No. 1.4e-08;  
Matches 21; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 8 LLEESQOQEKNEQELLELDKWANLWNWF 36  
|||:|||||:|||||  
Db 11 LLEQAQIQOQEKNEYELQKDKWASLWFW 39

## RESULT 15

US-11-112-277-34  
; Sequence 34, Application US/11112277  
; Publication No. US20050267293A1

## ; GENERAL INFORMATION:

; APPLICANT: Bousquet-Gagnon, Nathalie

; APPLICANT: Quraishi, Omar

; APPLICANT: Bridon, Dominique P.

; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN

; TITLE OF INVENTION: CONJUGATES

; FILE REFERENCE: 500862003700

; CURRENT APPLICATION NUMBER: US/11/112,277

; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/565,228

; PRIOR FILING DATE: 2004-04-23

; NUMBER OF SEQ ID NOS: 53

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 34

; LENGTH: 40

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: T1249 Analogue

; FEATURE:

; NAME/KEY: MOD\_RES

; LOCATION: 40

; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA

US-11-112-277-34

Query Match 59.5%; Score 119; DB 7; Length 40;  
Best Local Similarity 72.4%; Pred. No. 1.5e-08;  
Matches 21; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 8 LLEESQOQEKNEQELLELDKWANLWNWF 36  
|||:|||||:|||||  
Db 11 LLEQAQIQOQEKNEYELQKDKWASLWFW 39

Search completed: March 6, 2006, 15:54:21  
Job time : 10 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 16:12:57 ; Search time 117.333 Seconds  
(without alignments)  
134.809 Million cell updates/sec

Title: US-09-809-060A-3  
Perfect score: 36  
Sequence: 1 YGIIYNLEESQKQKNEQELLELDKWNLWVF 36

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Gapop 60.0 , Capext 60.0  
Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
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5: Geneseqp2002s:\*  
6: Geneseqp2003s:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	36	100.0	36	2	AAR98400 Peptide c
3	36	100.0	36	2	AAR17013 DP-178-li
4	36	100.0	36	4	AAB54787 HIV antiv
5	36	100.0	36	4	AAB52246 Virus rel
6	36	100.0	36	4	AAB78239 Core poly
7	36	100.0	36	4	AAB78240 Core poly
8	36	100.0	36	4	AAB70181 HIV viral
9	36	100.0	36	4	ABB02832 Viral cor
10	36	100.0	36	4	ABB02831 Viral cor
11	36	100.0	36	4	ABG67041 HIV-1 gp4
12	36	100.0	36	4	ABB01246 Viral DPl
13	36	100.0	36	4	ABB01247 Viral DPl
14	36	100.0	36	4	AAU13793 DP178-lik
15	36	100.0	36	4	AAU13792 DP178-lik
16	36	100.0	36	4	AAU14013 DP178 hom
17	36	100.0	36	5	AAO18773 HIV gp41
18	36	100.0	36	5	ADE02851 Hybrid po
19	36	100.0	36	5	ADE02852 Hybrid po
20	36	100.0	36	6	ABO10165 HIV1-RF g
21	36	100.0	36	8	ADN06924 Peptide #
22	36	100.0	36	8	ADS87259 HIV-1 gp4
23	36	100.0	36	9	ADY71494 HIV-1 tra
24	36	100.0	269	2	AAW22837 SEQ ID NO

25	36	100.0	269	5	ABG68308 Envelope
26	36	100.0	269	6	ABU57715 Human imm
27	36	100.0	861	2	AAW43074 HIV-1 gp1
28	36	100.0	865	1	ADP70175 Sequence
29	36	100.0	865	9	ADX39688 HIV Env p
30	36	100.0	866	1	AAP80966 HIV prote
31	31	86.1	35	3	AAW89838 Core poly
32	31	86.1	35	3	AAW89839 Core poly
33	27	75.0	225	8	ADU68214 gp41 ecto
34	27	75.0	849	9	ADX39678 HIV Env p
35	26	72.2	36	2	AAR67698 DP-178 ho
36	26	72.2	36	2	AAR98399 DP185 cor
37	26	72.2	36	2	AAW17012 DP-178-li
38	26	72.2	36	4	AAW67040 HIV-1 gp4
39	26	72.2	36	4	AAU14012 DP178 hom
40	26	72.2	38	7	ADK66257 Human imm
41	26	72.2	45	7	ADK66261 Human imm
42	26	72.2	48	8	ADU80506 Transmemb
43	26	72.2	48	9	ADZ40264 HIV-1 gp4
44	26	72.2	856	1	AAW61514 Sequence
45	26	72.2	856	2	AAW89325 HIV-1 env

#### ALIGNMENTS

#### RESULT 1

AAAR67699  
ID AAR67699 standard; peptide; 36 AA.  
XX AAR67699;  
AC AAR67699;  
XX  
XX 16-OCT-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 24-AUG-1995 (first entry)  
XX  
DE DP-178 homologue derived from HIV-1 RF has antiviral activity.  
XX  
KW antiviral activity; DP-178; DP-107; diagnostic; HIV-1LAI;  
KW human immunodeficiency virus; transmembrane protein; gp41; alpha helix;  
KW leucine zipper; DP-185.  
XX  
OS Human immunodeficiency virus; (RF isolate).  
XX  
PN WO9428920-A1.  
XX  
PD 22-DEC-1994.  
XX  
PF 07-JUN-1994; 94WO-US005739.  
XX  
PR 25-JUN-1993; 93US-00073028.  
XX  
PA (UYDU-) UNIV DUKE.  
XX  
PI Bolognesi DP, Matthews TJ, Wild CT, Barney SO, Lambert DM;  
PI Petteway SR;  
XX  
XX WPI; 1995-036105/05.  
XX  
XX Computer search generated synthetic peptides - are inhibitors of HIV transmission.  
XX  
XX Example; Fig 1; 182pp; English.  
XX  
CC This peptide is isolated from HIV-1 isolate RF, and is a homologue of the  
CC peptide DP-178. DP-178 corresponds to amino acids 638 to 673 of the HIV-1  
CC isolate LAI transmembrane protein gp41. It forms a putative alpha helix  
CC at the C-terminal end of the gp41 ectodomain, and complexes with DP-107  
CC (corresponds to amino acids 558-595) which contains a leucine zipper  
CC motif. The peptides complex via non-covalent protein-protein  
CC interactions, and possess anti-viral activity. The peptide inhibits  
CC transmission to uninfected cells, and can also be used as type and/or  
CC subtype specific diagnostic tools. (Updated on 25-MAR-2003 to correct PN

CC field.) (Updated on 16-OCT-2003 to standardise OS field)  
 XX Sequence 36 AA;  
 SQ

Query Match 100.0%; Score 36; DB 2; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36  
 |||||  
 Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

## RESULT 2

AAR98400

ID AAR98400 standard; peptide; 36 AA.

XX AAR98400;

XX

DT 16-OCT-2003 (revised)

DT 17-FEB-1997 (first entry)

XX

XX

DE Peptide corresponding to residues 638-673 of HIV-1(RF) gp41.

XX Antifusogenic activity; antiviral capability; coiled-coil peptide;

KW ALLMOTI5; 107x178x4; PLZIP search motif; viral transmission; HIV;

KW influenza virus; hepatitis B virus.

XX

OS Human immunodeficiency virus 1.

XX

XX

PN WO9619495-A1.

XX

XX

PD 27-JUN-1996.

XX

XX

PF 20-DEC-1995; 95WO-US016733.

XX

XX

PR 20-DEC-1994; 94US-00360107.

XX

PR 06-JUN-1995; 95US-00470896.

XX

XX

PA (UYDU-) UNIV DUKE.

PA (TRIM-) TRIMERIS INC.

XX

XX

PI Bolognesi DP, Matthews TJ, Wild CT, Barney S, Lambert DM;

PI Petteway SR, Langlois AJ;

XX

XX

DR WPI; 1996-309517/31.

XX

XX

PT Inhibiting viral transmission, e.g. HIV or RSV, to a cell - using an

PT isolated peptide recognised by an ALLMOTI5, 107x178x4 or PLZIP sequence

PT search motif.

XX

XX

PS Disclosure; Fig 1; 471pp; English.

XX

XX

CC The sequences given in AAR98398-408 represent peptides which exhibit

CC antifusogenic activity, antiviral capability and/or the ability to

CC modulate intracellular processes involving coiled-coil peptide

CC structures. These peptides are recognised by the ALLMOTI5, 107x178x4 and

CC PLZIP search motifs. These peptides may be used to inhibit the

CC transmission of a virus, pref. HIV, influenza virus, or hepatitis B

CC virus, to a cell. (Updated on 16-OCT-2003 to standardise OS field)

XX

XX

SQ Sequence 36 AA;

Query Match

Best Local Similarity 100.0%; Score 36; DB 2; Length 36;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

|||||

Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

|||||

RESULT 3

XX

XX

XX

XX

XX

AAW17013

ID AAW17013 standard; peptide; 36 AA.

XX

XX

AC AAW17013;

XX

DT 17-OCT-2003 (revised)

DT 01-JUL-1997 (first entry)

XX

XX

DE DP-178-like peptide useful for treatment of HIV infection.

XX

XX

KW HIV; SIV; human; simian immunodeficiency virus; glycoprotein 41;

KW transmembrane; antiviral; DP-178; DP-107; vaccine; inhibition;

KW replication; transmission.

XX

OS Human immunodeficiency virus 1; RF isolate.

XX

XX

PN WO9640191-A1.

XX

XX

PD 19-DEC-1996.

XX

XX

PF 06-JUN-1996; 96WO-US009499.

XX

XX

PR 07-JUN-1995; 95US-00481957.

XX

XX

PA (TRIM-) TRIMERIS INC.

XX

XX

PI Johnson RM, Lambert DM;

XX

XX

DR WPI; 1997-099886/09.

XX

XX

PT Compens. contg. DP-178 or DP-107 in combination with other therapeutic

PT agent - useful for treatment of HIV infection, esp. by inhibiting

PT replication or transmission of HIV.

XX

XX

PS Disclosure; Fig 1; 84pp; English.

XX

XX

CC AAW17012-W17016 are DP-178 homologues that are useful in the treatment of

CC HIV infection. DP-178 is a peptide corresponding to residues 638-673 of

CC HIV type 1 glycoprotein 41 (gp41) transmembrane protein. DP-178 and its

CC derivatives/homologues are used in combination with a therapeutic agent,

CC e.g. a reverse transcriptase, viral protease, cytolysis, glycosylation or

CC viral mRNA processing inhibitor or a nucleoside inhibitor. The peptides

CC work by inhibiting viral replication or inhibiting transmission. They may

CC also be used in vaccines for protecting against HIV infection. (Updated

CC on 17-OCT-2003 to standardise OS field)

XX

XX

SQ Sequence 36 AA;

Query Match

Best Local Similarity 100.0%; Score 36; DB 2; Length 36;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

XX

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

|||||

Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

|||||

RESULT 4

AAB54787

ID AAB54787 standard; peptide; 36 AA.

XX

XX

AC AAB54787;

XX

XX

DT 11-SEP-2003 (revised)

DT 05-MAR-2001 (first entry)

XX

XX

DE HIV antiviral activity exhibiting peptide SEQ ID NO:4.

XX

XX

KW Long lasting fusion peptide inhibitor; viral infection; antiviral;

KW antifusogenic; mobile blood component; measles virus; MeV; SIV;

KW simian immunodeficiency virus; human parainfluenza virus; HPIV; RSV;

KW human respiratory syncytial virus; human immunodeficiency virus; HIV.

XX

XX

OS Human immunodeficiency virus 1.  
PN WO200069902-A1.  
XX  
XX  
PD 23-NOV-2000.  
XX  
XX  
PF 17-MAY-2000; 2000WO-US013651.  
XX  
XX  
PF 17-MAY-1999; 99US-0134406P.  
XX  
XX  
PR 10-SEP-1999; 99US-0153406P.  
XX  
XX  
PA (CONJ-) CONJUCHEM INC.  
XX  
XX  
PI Bridon DP, Dufresne RP, Boudjellab N, Robitaille M, Milner PG;  
XX  
XX  
DR WPI; 2001-007496/01.  
XX  
XX  
XX A modified peptide and a reactive group which is reactive with amino  
PT groups, hydroxyl groups, or thiol groups on blood components to form  
PT stable covalent bonds useful for treatment of viral infections, e.g.  
PT human immunodeficiency virus.  
XX  
XX  
XX Claim 6; Page 173-174; 211pp; English.  
XX  
XX  
CC The present invention describes a modified anti-viral peptide (I)  
CC comprising a peptide that exhibits anti-viral activity and a reactive  
CC group which is reactive with amino groups, hydroxyl groups, or thiol  
CC groups on blood components to form stable covalent bonds. (I) has anti-  
CC viral and anti-fusogenic activities. (I) inhibits viral infection of  
CC cells by inhibiting cell-cell fusion or free virus infection or to reduce  
CC the level of membrane fusion events between two or more entities, e.g.,  
CC virus-cell or cell-cell, relative to the level of membrane fusion that  
CC occurs in the absence of the peptide. (I) is useful in the treatment of  
CC patients who are suffering from viral infection, e.g. HIV, RSV, HPIV,  
CC MeV, and SIV. (I) may be administered prophylactically to previously  
CC uninfected individuals. This is useful in cases where an individual has  
CC been subjected to a high risk of exposure to a virus. By bonding of long-  
CC lived components of the blood, such as immunoglobulin, serum albumin, red  
CC blood cells and platelets the activity is extended for days to weeks.  
CC This is due to improved stability in vivo and a reduced susceptibility to  
CC peptidase or protease degradation. This minimises the need for more  
CC frequent, or even continual, administration of the peptides. AAB54784 to  
CC AAB5431 represent peptides used in the exemplification of the present  
CC invention. (Updated on 11-SEP-2003 to standardise OS field)  
XX  
XX  
SQ Sequence 36 AA;  
Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQKQKNEQELLELDKWANLWNWF 36  
DB 1 YTGIIYNLLEESQKQKNEQELLELDKWANLWNWF 36  
RESULT 5  
AAB92246  
ID AAB92246 standard; peptide; 36 AA.  
XX  
AC AAB92246;  
XX  
DT 22-JUN-2001 (first entry)  
XX  
XX Virus related peptide SEQ ID NO:1422.  
XX  
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidyl; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX

PN WO200069900-A2.  
XX  
PD 23-NOV-2000.  
XX  
XX  
PF 17-MAY-2000; 2000WO-US013576.  
XX  
XX  
PR 17-MAY-1999; 99US-0134406P.  
XX  
XX  
PR 10-SEP-1999; 99US-0153406P.  
XX  
XX  
PR 15-OCT-1999; 99US-0159783P.  
XX  
XX  
PA (CONJ-) CONJUCHEM INC.  
XX  
XX  
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;  
XX  
XX  
DR WPI; 2001-112059/12.  
XX  
XX  
PT Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity.  
XX  
XX  
PS Disclosure; Page 662-663; 733pp; English.  
XX  
XX  
CC The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity in  
CC vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 36 AA;  
Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTGIIYNLLEESQKQKNEQELLELDKWANLWNWF 36  
DB 1 YTGIIYNLLEESQKQKNEQELLELDKWANLWNWF 36  
RESULT 6  
AAB78239  
ID AAB78239 standard; peptide; 36 AA.  
XX  
AC AAB78239;  
XX  
XX 19-APR-2001 (first entry)  
DT  
XX  
DE Core polypeptide T1407.  
XX  
XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;  
KW antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;  
KW fusion-related disorder; bacterial infection; viral infection.  
XX  
XX Unidentified.  
XX  
XX WO200103723-A1.  
PN  
XX 18-JAN-2001.  
PD  
XX 10-JUL-2000; 2000WO-US018772.  
PF  
XX 09-JUL-1999; 99US-00350641.  
PR

XX (TRIM-) TRIMERIS INC.  
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI; 2001-147136/15.  
XX  
XX New hybrid polypeptide, useful for preventing, treating and diagnosing  
XX e.g. viral infections, comprises an enhancer peptide linked to a core  
XX polypeptide.  
XX  
XX Disclosure; Page 58; 151pp; English.  
XX  
XX The present sequence is a core polypeptide which may be linked to an  
XX enhancer peptide to form a novel hybrid polypeptide. The hybrid  
XX polypeptide exhibits enhanced pharmacokinetic properties relative to  
XX those exhibited by the core polypeptide when introduced into a living  
XX system. It is used to increase the in vitro or ex vivo half-life of the  
XX core polypeptide. The hybrid and core polypeptides can be used for  
XX modulating fusogenic events and intracellular processes involving coiled-  
XX coil peptide interactions. Other uses include preventing, treating and/or  
XX diagnosing disorders involving fusion events (e.g. modulation of  
XX neurotransmitter exchange and sperm-egg fusion), intracellular processes  
XX involving coiled-coil peptides (e.g. bacterial infections) and viral  
XX infections that involve cell-cell and/or virus-cell fusion (e.g. viral  
XX infections caused by human immunodeficiency virus, respiratory syncytial  
XX virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and  
XX polio virus). The enhancer peptide sequence increases the half-life and  
XX reduces the clearance rate of therapeutic peptides, which increases their  
XX efficacy and minimises the incidence and severity of adverse side  
XX effects. In addition, this increases the sensitivity of the diagnostic  
XX procedure in which they are used  
XX  
XX Sequence 36 AA;  
XX  
XX Query Match 100.0%; Score 36; DB 4; Length 36;  
XX Best Local Similarity 100.0%; Pred. No. 2e-27;  
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 YTGIIYNLLEESQKQKNEQELLELDKRWANLWNWF 36  
XX |||||||||||||||||||||||||||||||||||  
XX 1 YTGIIYNLLEESQKQKNEQELLELDKRWANLWNWF 36  
XX  
XX  
XX RESULT 7  
XX AAB78240  
XX ID AAB78240 standard; peptide; 36 AA.  
XX AC AAB78240;  
XX DT 19-APR-2001 (first entry)  
XX DE Core polypeptide T1408.  
XX  
XX Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;  
XX antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;  
XX fusion-related disorder; bacterial infection; viral infection.  
XX  
XX Unidentified.  
XX  
XX WO200103723-A1.  
XX  
XX 18-JAN-2001.  
XX  
XX 10-JUL-2000; 2000WO-US018772.  
XX  
XX 09-JUL-1999; 99US-00350641.  
XX  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI; 2001-147136/15. ;  
XX  
XX

XX New hybrid polypeptide, useful for preventing, treating and diagnosing  
XX e.g. viral infections, comprises an enhancer peptide linked to a core  
XX polypeptide.  
XX  
XX Disclosure; Page 58; 151pp; English.  
XX  
XX The present sequence is a core polypeptide which may be linked to an  
XX enhancer peptide to form a novel hybrid polypeptide. The hybrid  
XX polypeptide exhibits enhanced pharmacokinetic properties relative to  
XX those exhibited by the core polypeptide when introduced into a living  
XX system. It is used to increase the in vitro or ex vivo half-life of the  
XX core polypeptide. The hybrid and core polypeptides can be used for  
XX modulating fusogenic events and intracellular processes involving coiled-  
XX coil peptide interactions. Other uses include preventing, treating and/or  
XX diagnosing disorders involving fusion events (e.g. modulation of  
XX neurotransmitter exchange and sperm-egg fusion), intracellular processes  
XX involving coiled-coil peptides (e.g. bacterial infections) and viral  
XX infections that involve cell-cell and/or virus-cell fusion (e.g. viral  
XX infections caused by human immunodeficiency virus, respiratory syncytial  
XX virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and  
XX polio virus). The enhancer peptide sequence increases the half-life and  
XX reduces the clearance rate of therapeutic peptides, which increases their  
XX efficacy and minimises the incidence and severity of adverse side  
XX effects. In addition, this increases the sensitivity of the diagnostic  
XX procedure in which they are used  
XX  
XX Sequence 36 AA;  
XX  
XX Query Match 100.0%; Score 36; DB 4; Length 36;  
XX Best Local Similarity 100.0%; Pred. No. 2e-27;  
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 YTGIIYNLLEESQKQKNEQELLELDKRWANLWNWF 36  
XX |||||||||||||||||||||||||||||||||||  
XX 1 YTGIIYNLLEESQKQKNEQELLELDKRWANLWNWF 36  
XX  
XX  
XX RESULT 8  
XX AAU70181  
XX ID AAU70181 standard; peptide; 36 AA.  
XX AC AAU70181;  
XX DT 14-FEB-2002 (first entry)  
XX DE HIV viral envelope protein stabilising peptide #3.  
XX  
XX Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;  
XX anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;  
XX alpha-helical region; ectodomain.  
XX  
XX Homo sapiens.  
XX  
XX WO200170262-A2.  
XX  
XX 27-SEP-2001.  
XX  
XX 15-MAR-2001; 2001WO-US008108.  
XX  
XX 17-MAR-2000; 2000US-0189981P.  
XX  
XX (PANA-) PANACOS PHARM INC.  
XX  
XX Wild CT, Allaway GP;  
XX  
XX WPI; 2001-626098/72.  
XX  
XX Immunogenic composition for inhibiting HIV infection, comprises viral  
XX envelope protein or its fragment exterior to viral membrane, a  
XX stabilizing peptide, and, optionally, viral cell surface receptor or its  
XX fragment.  
XX  
XX

PS Claim 6; Page 45; 84pp; English.

XX The invention relates to methods of generating immunogens that elicit  
 CC neutralising antibodies which target regions of viral envelope proteins  
 CC such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-  
 CC 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and  
 CC AAU70677-AAU70743 represent stabilising peptides modelling the alpha-  
 CC helical regions of the ectodomain of the HIV-1 transmembrane protein to  
 CC stabilise fusion-active intermediate structures, which can be used as  
 CC vaccine immunogens. Immunogenic compositions comprise a viral envelope  
 CC protein or its fragment exterior to the viral membrane, a stabilising  
 CC peptide to disrupt formation of structural intermediates necessary for  
 CC viral fusion and entry, and optionally, a viral cell surface receptor or  
 CC its fragment. The stabilising peptide is capable of associating with the  
 CC envelope protein or its fragment to form a stabilised, fusion active  
 CC structure. Antibody binding assays are used to determine the ability of  
 CC immunogen vaccines to generate an immune response to various forms of  
 CC envelope. Virus neutralisation assays can be used to characterise the  
 CC antibody response raised against HIV-1 gp41 domains. The sequences and  
 CC methods are useful for inhibiting HIV infection, for inducing an immune  
 CC response in an animal and for raising antibodies

XX  
 SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOQKEQELLELDKRWANLWNWF 36  
 |||||  
 DB 1 YTGIIYNLLEESQNOQKEQELLELDKRWANLWNWF 36  
 |||||

RESULT 9

ABB02832

ID ABB02832 standard; peptide; 36 AA.

XX  
 AC ABB02832;

XX  
 DT 11-SEP-2003 (revised)  
 DT 06-AUG-2003 (revised)  
 DT 03-JAN-2002 (first entry)

XX  
 DE Viral core polypeptide, SEQ ID NO: 1359.

XX  
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.

XX  
 OS Viruses.

XX  
 PN WO200164013-A2.

XX  
 PD 07-SEP-2001.

XX  
 PF 07-FEB-2001; 2001WO-US003988.

XX  
 PR 29-FEB-2000; 2000US-00515965.

XX  
 PA (TRIM-) TRIMERIS INC.

XX  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI; 2001-514829/56.

XX  
 DR Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection.

XX  
 PS Disclosure; Page 525; 587pp; English.

XX  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI; 2001-514829/56.

XX  
 DR Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection.

XX  
 PS Disclosure; Page 525; 587pp; English.

XX  
 XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-

CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
 CC regions of proteins interact non-covalently with each other and/or with  
 CC peptides derived from them. This interaction is required for normal  
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
 CC peptide analogues may be used to inhibit respiratory syncytial virus  
 CC (RSV) infection in a cell. They may also be used to inhibit HIV  
 CC infection. The present sequence is a peptide provided in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
 CC 11-SEP-2003 to standardise OS field)

XX  
 SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2e-27;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YTGIIYNLLEESQNOQKEQELLELDKRWANLWNWF 36  
 |||||  
 DB 1 YTGIIYNLLEESQNOQKEQELLELDKRWANLWNWF 36  
 |||||

RESULT 10

ABB02831

ID ABB02831 standard; peptide; 36 AA.

XX  
 AC ABB02831;

XX  
 DT 11-SEP-2003 (revised)  
 DT 06-AUG-2003 (revised)  
 DT 03-JAN-2002 (first entry)

XX  
 DE Viral core polypeptide, SEQ ID NO: 1358.

XX  
 KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
 KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
 KW infection.

XX  
 OS Viruses.

XX  
 PN WO200164013-A2.

XX  
 PD 07-SEP-2001.

XX  
 PF 07-FEB-2001; 2001WO-US003988.

XX  
 PR 29-FEB-2000; 2000US-00515965.

XX  
 PA (TRIM-) TRIMERIS INC.

XX  
 PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
 XX WPI; 2001-514829/56.

XX  
 DR Heptad repeat region peptide analogs useful for inhibiting virus/cells  
 PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
 PT infection.

XX  
 PS Disclosure; Page 524-525; 587pp; English.

XX  
 XX The invention relates to isolated analogues of the heptad repeat region  
 CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
 CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
 CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
 CC regions of proteins interact non-covalently with each other and/or with  
 CC peptides derived from them. This interaction is required for normal  
 CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
 CC peptide analogues may be used to inhibit respiratory syncytial virus  
 CC (RSV) infection in a cell. They may also be used to inhibit HIV  
 CC infection. The present sequence is a peptide provided in the  
 CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
 CC 11-SEP-2003 to standardise OS field)

## SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36  
|||||  
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36

## RESULT 11

AAG67041  
ID AAG67041 standard; peptide; 36 AA.

AC AAG67041;  
XX  
DT 11-SEP-2003 (revised)  
DT 03-JAN-2002 (first entry)  
XX  
DE HIV-1 gp41 peptide DP178 homologue DP-185.  
XX  
KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
KW infection; DP185.  
XX  
OS Human immunodeficiency virus 1.  
XX  
PN WO200164013-A2.  
XX  
PD 07-SEP-2001.  
XX  
PF 07-FEB-2001; 2001WO-US003988.  
XX  
PR 29-FEB-2000; 2000US-00515965.  
XX

PA (TRIM-) TRIMERIS INC.

PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
DR WPI; 2001-514829/56.  
XX  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection.  
XX  
PS Example; Fig 1; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
CC regions of proteins interact non-covalently with each other and/or with  
CC peptides derived from them. This interaction is required for normal  
CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
CC peptide analogues may be used to inhibit respiratory syncytial virus  
CC (RSV) infection in a cell. They may also be used to inhibit HIV  
CC infection. The present sequence is a peptide provided in the  
CC specification. (Updated on 11-SEP-2003 to standardise OS field)

## SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36  
|||||  
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36

## RESULT 12

ABB01246

ID ABB01246 standard; peptide; 36 AA.

AC ABB01246;  
XX  
DT 11-SEP-2003 (revised)  
DT 06-AUG-2003 (revised)  
DT 03-JAN-2002 (first entry)  
XX  
DE Viral DP178/107-like region peptide T1407.  
XX  
KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;  
KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;  
KW infection.  
XX  
OS Viruses.

XX  
FH Key Location/Qualifiers  
FT Modified-site 1  
FT Modified-site 36 /note= "N-terminal is substituted by Ac"  
FT Modified-site 36 /note= "C-terminal amide"  
XX

PN WO200164013-A2.

XX  
PD 07-SEP-2001.

PF 07-FEB-2001; 2001WO-US003988.

XX  
PR 29-FEB-2000; 2000US-00515965.

XX  
PA (TRIM-) TRIMERIS INC.

PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
DR WPI; 2001-514829/56.

XX  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
PT fusion, useful for treating HIV and Respiratory Syncytial Virus  
PT infection.  
XX  
PS Disclosure; Page 58; 587pp; English.

XX The invention relates to isolated analogues of the heptad repeat region  
CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
CC regions of proteins interact non-covalently with each other and/or with  
CC peptides derived from them. This interaction is required for normal  
CC infectivity of viruses such as RSV and HIV. The heptad repeat region  
CC peptide analogues may be used to inhibit respiratory syncytial virus  
CC (RSV) infection in a cell. They may also be used to inhibit HIV  
CC infection. The present sequence is a peptide provided in the  
CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
CC 11-SEP-2003 to standardise OS field)

## SQ Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36  
|||||  
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQANLWNWF 36

## RESULT 13

ABB01247

ID ABB01247 standard; peptide; 36 AA.

XX ABB01247;

XX ABB01247;

DT 11-SEP-2003 (revised)







GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:19:28 ; Search time 19 Seconds  
(without alignments)  
182.305 Million cell updates/sec

Title: US-09-809-060A-3  
Perfect score: 36  
Sequence: 1 YGIIYNLLESQNKQKNEQLLELDKWNLNWNP 36

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	72.2	856	1 VCLJVL	env polyprotein pr
2	23	63.9	855	1 VCLJAJ	env polyprotein pr
3	21	58.3	357	2 S21994	envelope protein g
4	21	58.3	357	2 S21996	envelope protein g
5	21	58.3	443	2 C41621	env polyprotein p
6	21	58.3	847	2 T09448	envelope glycoprot
7	21	58.3	847	2 S13289	env protein - huma
8	21	58.3	851	2 S33985	env polyprotein -
9	21	58.3	854	2 S13288	env protein - huma
10	21	58.3	856	1 VCLJ3W	env polyprotein pr
11	21	58.3	856	1 VCLJH3	env polyprotein pr
12	21	58.3	861	1 VCLJSC	env polyprotein pr
13	21	58.3	861	1 VCLJLV	env polyprotein pr
14	19	52.8	357	2 S21992	envelope protein g
15	19	52.8	358	2 S21998	envelope protein g
16	16	44.4	853	2 S54384	env polyprotein p
17	16	44.4	855	1 VCLJZR	env polyprotein pr
18	16	44.4	859	1 VCLJMN	env polyprotein pr
19	15	41.7	357	2 S22004	envelope protein g
20	15	41.7	357	2 S22006	envelope protein g
21	13	36.1	357	2 S21990	envelope protein g
22	13	36.1	843	1 H44001	env polyprotein pr
23	13	36.1	852	1 T12016	envelope glycoprot
24	12	33.3	358	2 S70417	envelope protein g
25	12	33.3	358	2 S22000	envelope protein g
26	12	33.3	358	2 S22002	envelope protein g
27	12	33.3	445	2 A41621	env polyprotein M
28	12	33.3	454	2 B41621	env polyprotein D
29	12	33.3	729	1 VCLJFK	env polyprotein pr

30 12 33.3 861 1 VCLJKB env polyprotein pr  
31 11 30.6 856 1 A44963 env polyprotein pr  
32 10 27.8 868 1 VCLJH4 env polyprotein -  
33 9 25.0 846 1 VCLJND env polyprotein pr  
34 9 25.0 852 1 VCLJBR env polyprotein -  
35 9 25.0 859 2 T01672 envelope polyprote  
36 8 22.2 592 2 T03682 catechol oxidase (  
37 8 22.2 596 1 S33540 catechol oxidase (  
38 8 22.2 599 2 T07097 catechol oxidase (  
39 7 19.4 136 2 JU0266 envelope polyprote  
40 7 19.4 136 2 JT0954 envelope polyprote  
41 7 19.4 198 2 T46082 hypotetical prote  
42 7 19.4 297 2 C90179 cysteine synthase  
43 7 19.4 425 2 T19415 hypotetical prote  
44 7 19.4 426 2 G69933 glutamate dehydrog  
45 7 19.4 426 2 T01790 protoporphyrin IX

#### ALIGNMENTS

##### RESULT 1

VCLJVL  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)  
N;Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C:Accession: A03974  
R:Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.  
Nature 313, 450-458, 1985  
A:Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi:  
A:Reference number: A93355; MUID:85111157; PMID:2982104  
A:Accession: A03974  
A:Molecule type: DNA  
A:Residues: 1-856 <MUE>  
A:Cross-references: UNIPROT:P03376; UNIPARC:UPI000012A01F; GB:K02083; NID:g555008; PIDN:  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprote  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>  
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,  
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Aen)  
Query Match 72.2%; Score 26; DB 1; Length 856;  
Best Local Similarity 100.0%; Pred. No. 1.2e-17;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 BESQOQKNEQLLELDKWNLNW 35  
DB 647 BESQOQKNEQLLELDKWNLNW 672

##### RESULT 2

VCLJAJ  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
N;Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A:Note: host Homo sapiens (man)  
C:Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C:Accession: A03976  
R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Shi  
Science 227, 484-492, 1985  
A:Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453; PMID:2578227  
A:Accession: A03976  
A:Molecule type: DNA  
A:Residues: 1-855 <SAN>  
A:Cross-references: UNIPROT:P03378; UNIPARC:UPI000012A00F; GB:K02007; NID:g328658; PIDN:  
C:Genetics:

```
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>
F:510-855/Product: transmembrane glycoprotein #status predicted <TM>
F:87,129,140,150,184,190,200,244,265,298,304,334,341,358,364,388,394,400,408,445,458
F:610,624,636,815/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          53.9%; Score 23; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 1e-14;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLEESQSQKNEQELLELDKWA 30
   |||||
Db 644 LLEESQSQKNEQELLELDKWA 666

RESULT 3
S21994
envelope protein gp120/gp41 - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
A:Variety: isolate 27B
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S21994; S70421
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.
submitted to the EMBL Data Library, July 1991
A:Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined
A:Reference number: S21990
A:Accession: S21994
A:Molecule type: DNA
A:Residues: 1-357 <STEL>
A:Cross-references: UNIPROT:Q78118; UNIPARC:UPI0000178606; EMBL:X61355; NID:g60179; PIDN:
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70421
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140, 'X', 142-312, 'X', 314-357 <STR2>
A:Cross-references: UNIPARC:UPI0000FF05F; EMBL:X61355; NID:g60179
C:Superfamily: type E retrovirus env polyprotein

Query Match          58.3%; Score 21; DB 2; Length 357;
Best Local Similarity 100.0%; Pred. No. 3.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQSQKNEQELLELDKWA 30
   |||||
Db 148 EESQSQKNEQELLELDKWA 168

RESULT 4
S21996
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S70422; S21996
R:Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
AIDS Res. Hum. Retroviruses 8, 53-59, 1992
A:Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal
A:Reference number: S70417; MUID:92144209; PMID:1736940
A:Accession: S70422
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-357 <ST2>
A:Cross-references: UNIPROT:Q78119; UNIPARC:UPI0000104EC6; EMBL:X61356; NID:g60181; PIDN:
A:Experimental source: patient 27L
A:Note: submitted to the EMBL Data Library, July 1991
C:Superfamily: type E retrovirus env polyprotein

Query Match          58.3%; Score 21; DB 2; Length 357;
S13289
```

```
Best Local Similarity 100.0%; Pred. No. 3.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQSQKNEQELLELDKWA 30
   |||||
Db 148 EESQSQKNEQELLELDKWA 168

RESULT 5
C41621
env polyprotein P - human immunodeficiency virus type 1 (fragment)
N:Alternate names: coat protein
N:Contains: amino end of coat protein gp41; carboxyl end of coat protein gp120
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 11-Feb-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C:Accession: C41621
R:Burger, H.; Weiser, B.; Flaherty, K.; Gulla, J.; Nguyen, P.N.; Gibbs, R.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 11236-11240, 1991
A:Title: Evolution of human immunodeficiency virus type 1 nucleotide sequence diversity
A:Reference number: A41621; MUID:92107924; PMID:1763038
A:Accession: C41621
A:Molecule type: DNA
A:Residues: 1-443 <BUR>
A:Cross-references: UNIPROT:Q80023; UNIPARC:UPI0000104256; GB:M77230; NID:g328631; PIDN:
A:Note: this virus was isolated from the mother's sexual partner
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F:1-251/Product: coat protein gp120 (fragment) #status predicted <GP1>
F:252-443/Product: coat protein gp41 (fragment) #status predicted <GP2>
F:424-443/Domain: transmembrane #status predicted <TM>
F:9,23,36,48,78,101,107,131,137,143,147,153,188,200,203,351,356,365,377/Binding site: ca

Query Match          58.3%; Score 21; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 4.8e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQSQKNEQELLELDKWA 30
   |||||
Db 387 EESQSQKNEQELLELDKWA 407

RESULT 6
T09448
envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09448
R:Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,
submitted to the EMBL Data Library, July 1996
A:Reference number: Z16673
A:Accession: T09448
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-847 <PAN>
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI000010C516; EMBL:U63632; NID:g1465777; PII
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein

Query Match          58.3%; Score 21; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 8.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQSQKNEQELLELDKWA 30
   |||||
Db 638 EESQSQKNEQELLELDKWA 658

RESULT 7
S13289
```

```
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S13289
R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13289
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-847 <OBR>
A:Cross-references: UNIPROT:Q75760; UNIPARC:UPI000017861B
C:Superfamily: type E retrovirus env polyprotein

Query Match 58.3%; Score 21; DB 2; Length 847;
Best Local Similarity 100.0%; Pred. No. 8.9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWA 30
Db 638 EESQNOQEKNEQELLELDKWA 658

RESULT 8
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S33985
R/Carlini, F.
submitted to the EMBL Data Library, November 1991
A:Reference number: S33979
A:Accession: S33985
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-851 <CAR>
A:Cross-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:Z11530; NID:g60192; PIDN
C:Superfamily: type E retrovirus env polyprotein

Query Match 58.3%; Score 21; DB 2; Length 851;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWA 30
Db 642 EESQNOQEKNEQELLELDKWA 662

RESULT 9
env protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Dec-2004
C:Accession: S13288
R/O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OBR>
A:Cross-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:Q90178; UNIPROT:Q78243; UNIP
C:Superfamily: type E retrovirus env polyprotein

Query Match 58.3%; Score 21; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWA 30
Db 645 EESQNOQEKNEQELLELDKWA 665
```

```
RESULT 10
VCJ3W
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
C:Accession: A24774
R/Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, B.S
Cell 45, 637-648, 1986
A:Title: Identification and characterization of conserved and variable regions in the en
A:Reference number: A24774; MUID:86218077; PMID:2423250
A:Accession: A24774
A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: UNIPROT:P31872; UNIPARC:UPI000012A024; GB:K03455; GB:M38432; NID:g191
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GP1>
F:502-847/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459,
Query Match 58.3%; Score 21; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWA 30
Db 647 EESQNOQEKNEQELLELDKWA 667

RESULT 11
VCJ3H3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03973
R/Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dorar
Nberger, J.A.; Papas, T.S.; Graybe, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K0200
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TM>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict
Query Match 58.3%; Score 21; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQNOQEKNEQELLELDKWA 30
Db 647 EESQNOQEKNEQELLELDKWA 667

RESULT 12
VCJ3SC
env polyprotein precursor - human immunodeficiency virus type 1 (isolate SC)
```

N;Alternate names: coat polyprotein  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 16-Feb-1997  
C;Accession: B28922  
R;Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, B.; Farrell, K.; Wong-Staal, A.; Weiss, R.A.; Johnson, V.A.; et al. 1988  
Virology 164, 531-536, 1988  
A;Title: Envelope sequences of two new United States HIV-1 isolates.  
A;Reference number: A28922; MUID:88219542; PMID:3369091  
A;Accession: B28922  
A;Molecule type: DNA  
A;Residues: 1-861 <GUR>  
A;Cross-references: UNIPARC:UPI0000174A39  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: capsid protein; coat protein; glycoprotein; polyprotein; transmembrane protein  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-861/Product: env polyprotein #status predicted <EP>  
F;87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 58.3%; Score 21; DB 1; Length 861;  
Best Local Similarity 100.0%; Pred. No. 9.1e-13;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30  
|||||  
Db 652 EESQOQEKNEQELLELDKWA 672

RESULT 13  
VCILJLV  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate LAV-1a)  
N;Alternate names: coat polyprotein  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Note: host Homo sapiens (man)  
C;Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C;Accession: A03975  
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.  
Cell 40, 9-17, 1985  
A;Title: Nucleotide sequence of the AIDS virus, LAV.  
A;Reference number: A90866; MUID:85099333; PMID:2981635  
A;Accession: A03975  
A;Molecule type: DNA  
A;Residues: 1-861 <WAI>  
A;Cross-references: UNIPROT:P03377; UNIPARC:UPI000012A013; GB:K02013; NID:G326417; PIDN:  
C;Genetics:  
A;Gene: env  
C;Superfamily: type E retrovirus env polyprotein  
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein  
F;1-30/Domain: signal sequence #status predicted <SIG>  
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>  
F;517-861/Product: transmembrane glycoprotein #status predicted <TM>  
F;88,136,141,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411  
F;616,621,630,642,679,755,821/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 58.3%; Score 21; DB 1; Length 861;  
Best Local Similarity 100.0%; Pred. No. 9.1e-13;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30  
|||||  
Db 652 EESQOQEKNEQELLELDKWA 672

RESULT 14  
S21992  
envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)  
C;Species: human immunodeficiency virus type 1, HIV-1  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S70424; MUID:8219542; PMID:3369091  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A;Reference number: S70417; MUID:92144209; PMID:1736940  
A;Accession: S70424  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-357 <ST2>  
A;Cross-references: UNIPROT:Q78112; UNIPARC:UPI0000107A48; EMBL:X61359; NID:G60177; PIDN:  
A;Experimental source: patient 22  
A;Note: submitted to the EMBL Data Library, July 1991  
C;Superfamily: type E retrovirus env polyprotein

Query Match 52.8%; Score 19; DB 2; Length 357;  
Best Local Similarity 100.0%; Pred. No. 3.5e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SQNQEKNEQELLELDKWA 30  
|||||  
Db 150 SQNQEKNEQELLELDKWA 168

RESULT 15  
S21998  
envelope protein gp120/gp41 - human immunodeficiency virus type 1  
C;Species: human immunodeficiency virus type 1, HIV-1  
A;Variety: isolate 28  
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C;Accession: S21998; S70425  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.  
submitted to the EMBL Data Library, July 1991  
A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined by PCR  
A;Reference number: S21990  
A;Accession: S21998  
A;Molecule type: DNA  
A;Residues: 1-358 <STE1>  
A;Cross-references: UNIPROT:Q78120; UNIPARC:UPI0000178607; EMBL:X61359; NID:G60182; PIDN:  
R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.  
AIDS Res. Hum. Retroviruses 8, 53-59, 1992  
A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid  
A;Reference number: S70417; MUID:92144209; PMID:1736940  
A;Accession: S70425  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-222, 'X', 224-358 <STE2>  
A;Cross-references: UNIPARC:UPI00000FE72C; EMBL:X61359; NID:G60182; PIDN:CAA43630.1; PID:  
C;Superfamily: type E retrovirus env polyprotein

Query Match 52.8%; Score 19; DB 2; Length 358;  
Best Local Similarity 100.0%; Pred. No. 3.5e-11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 SQNQEKNEQELLELDKWA 30  
|||||  
Db 151 SQNQEKNEQELLELDKWA 169

Search completed: March 6, 2006, 16:26:19  
Job time : 19 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:13:17 ; Search time 122 Seconds  
(without alignments)  
208.189 Million cell updates/sec

Title: US-09-809-060A-3  
Perfect score: 36  
Sequence: 1 YGIYIYLLSESQKQKNEQELLELDKXANLWNF 36

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Uniprot\_05\_80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	865	1 ENV_HV1RH	P04579 human immun
2	33	91.7	122	2 Q90DJ7_9HIV1	Q90DJ7 human immun
3	32	88.9	120	2 Q4VUS2_9HIV1	Q4VUS2 human immun
4	32	88.9	122	2 Q6WH26_9HIV1	Q6WH26 human immun
5	32	88.9	122	2 Q9QIW9_9HIV1	Q9QIW9 human immun
6	32	88.9	143	2 Q53I38_9HIV1	Q53I38 human immun
7	32	88.9	848	2 Q6UYP3_9HIV1	Q6UYP3 human immun
8	32	88.9	848	2 Q6UYP4_9HIV1	Q6UYP4 human immun
9	32	88.9	849	2 Q6UYP5_9HIV1	Q6UYP5 human immun
10	32	88.9	849	2 Q6UYP7_9HIV1	Q6UYP7 human immun
11	32	88.9	849	2 Q6UYP8_9HIV1	Q6UYP8 human immun
12	32	88.9	849	2 Q6UYP9_9HIV1	Q6UYP9 human immun
13	32	88.9	849	2 Q6UYP3_9HIV1	Q6UYP3 human immun
14	32	88.9	849	2 Q6UYP5_9HIV1	Q6UYP5 human immun
15	32	88.9	849	2 Q6UYP6_9HIV1	Q6UYP6 human immun
16	32	88.9	850	2 Q6UYP0_9HIV1	Q6UYP0 human immun
17	32	88.9	850	2 Q6UYP1_9HIV1	Q6UYP1 human immun
18	32	88.9	850	2 Q6UYP2_9HIV1	Q6UYP2 human immun
19	32	88.9	850	2 Q6UYP7_9HIV1	Q6UYP7 human immun
20	32	88.9	850	2 Q6UYP8_9HIV1	Q6UYP8 human immun
21	32	88.9	850	2 Q6UYP9_9HIV1	Q6UYP9 human immun
22	32	88.9	851	2 Q6UYP4_9HIV1	Q6UYP4 human immun
23	32	88.9	851	2 Q6UYP5_9HIV1	Q6UYP5 human immun
24	32	88.9	851	2 Q6UYP6_9HIV1	Q6UYP6 human immun
25	32	88.9	851	2 Q6UYP7_9HIV1	Q6UYP7 human immun
26	32	88.9	851	2 Q6UYP8_9HIV1	Q6UYP8 human immun
27	32	88.9	853	2 Q6UYP9_9HIV1	Q6UYP9 human immun
28	32	88.9	854	2 Q6UYP0_9HIV1	Q6UYP0 human immun
29	32	88.9	854	2 Q6UYP3_9HIV1	Q6UYP3 human immun
30	32	88.9	856	2 Q6UYP4_9HIV1	Q6UYP4 human immun
31	32	88.9	856	2 Q6UYP5_9HIV1	Q6UYP5 human immun

32	32	88.9	856	2	Q6UYZ3_9HIV1	Q6UYZ3 human immun
33	32	88.9	857	2	Q6UZ32_9HIV1	Q6UZ32 human immun
34	32	88.9	857	2	Q6UZ33_9HIV1	Q6UZ33 human immun
35	32	88.9	858	2	Q6UYZ9_9HIV1	Q6UYZ9 human immun
36	32	88.9	858	2	Q6UZ31_9HIV1	Q6UZ31 human immun
37	32	88.9	859	2	Q6UYR8_9HIV1	Q6UYR8 human immun
38	32	88.9	859	2	Q6UYR9_9HIV1	Q6UYR9 human immun
39	32	88.9	859	2	Q6UYR0_9HIV1	Q6UYR0 human immun
40	32	88.9	859	2	Q6UYR1_9HIV1	Q6UYR1 human immun
41	32	88.9	859	2	Q6UYR2_9HIV1	Q6UYR2 human immun
42	32	88.9	859	2	Q6UYR3_9HIV1	Q6UYR3 human immun
43	32	88.9	859	2	Q6UYR4_9HIV1	Q6UYR4 human immun
44	32	88.9	859	2	Q6UYR5_9HIV1	Q6UYR5 human immun
45	32	88.9	859	2	Q6UYR6_9HIV1	Q6UYR6 human immun

## ALIGNMENTS

RESULT 1						
ENV_HV1RH	AC	P04579;	DT	13-AUG-1987 (rel. 05, Created)	STANDARD;	PRT; 865 AA.
DT	13-AUG-1987 (rel. 05, Last sequence update)					
DT	13-SEP-2005 (rel. 48, Last annotation update)					
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].					
GN	Names=ENV;					
OS	Human immunodeficiency virus type 1 (isolate RF/HAT) (HIV-1).					
OC	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;					
OC	Lentivirus; Primate lentivirus group.					
OX	NCBI_TaxID=11701;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE [GENOMIC RNA].					
RX	MEDLINE=86218077; PubMed=2423250; DOI=10.1016/0092-8674(86)90778-6;					
RA	Starcich B.R., Hahn B.H., Shaw G.M., McNeely P.D., Modrow S., Wolf H.,					
RA	Parks E.S., Parks W.P., Josephs S.F., Gallo R.C., Wong-Staal F.;					
RT	"Identification and characterization of conserved and variable regions in the envelope gene of HTLV-III/LAV, the retrovirus of AIDS.";					
RL	Cell 45:637-648(1986).					
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.					
CC	EMBL; M17451; AAA45057.1; -, Genomic_RNA.					
DR	HSSP; P04578; 1DLB.					
DR	SMR; P04579; 549-635.					
DR	HIV; M17451; ENVSRF.					
DR	InterPro; IPR000328; Env GP41.					
DR	InterPro; IPR000777; GP120.					
DR	Pfam; PF00516; GP120; 1.					
DR	Pfam; PF00517; GP41; 1.					
KW	AIDS; Capsid protein; Glycoprotein; Polyprotein; Signal;					
KW	Structural protein; Transmembrane.					
FT	SIGNAL 1 29					
FT	CHAIN 30 539					
FT	CHAIN 520 865					
FT	CARBOHYD 87 87					
FT	CARBOHYD 129 129					
FT	CARBOHYD 136 136					
FT	CARBOHYD 139 139					
FT	CARBOHYD 156 156					
FT	CARBOHYD 193 193					
FT	CARBOHYD 194 194					
FT	CARBOHYD 197 197					
FT	CARBOHYD 198 198					
FT	CARBOHYD 203 203					
FT	CARBOHYD 210 210					
FT	CARBOHYD 247 247					

FT CARBOHYD 254 254 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 275 275 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 289 289 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 302 302 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 308 308 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 314 314 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 344 344 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 351 351 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 367 367 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 397 397 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 403 403 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 407 407 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 413 413 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 418 418 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 455 455 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 471 471 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 620 620 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 625 625 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 634 634 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 646 646 N-linked (GLNAC. . .) (Potential).  
FT CARBOHYD 825 825 N-linked (GLNAC. . .) (Potential).  
FT DISULFID 53 73 By similarity.  
FT DISULFID 118 218 By similarity.  
FT DISULFID 125 209 By similarity.  
FT DISULFID 130 157 By similarity.  
FT DISULFID 231 260 By similarity.  
FT DISULFID 241 252 By similarity.  
FT DISULFID 309 343 By similarity.  
FT DISULFID 389 452 By similarity.  
FT DISULFID 396 425 By similarity.  
SQ SEQUENCE 865 AA; 97809 MW; 28828BC2314ADCAC CRC64;

Query Match 100.0%; Score 36; DB 1; Length 865;  
Best Local Similarity 100.0%; Pred. No. 2.9e-26;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQOQEKNEQELLELDKQWNLWNWF 36  
DB 647 YTGIIYNLEESQOQEKNEQELLELDKQWNLWNWF 682

RESULT 2  
Q90DJ7\_9HIV1 PRELIMINARY; PRT; 122 AA.  
AC Q90DJ7\_9HIV1 PRELIMINARY; PRT; 122 AA.  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN-UG;  
RA Hu D.J., Baggs J., Downing R.G., Pieniazek D., Dorn J., Fridlund C.,  
RA Biryahwaho B., Sempaia S.D.K., Rayfield M.A., Dondero T.J., Lal R.,  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF307734; AAL08795.1; -; Genomic\_DNA.  
DR HSP; P04624; 1JAU.  
DR SMR; Q90DJ7; 1-105.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_GP41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 122  
SQ SEQUENCE 122 AA; 14743 MW; FBB3D55A1B1482A2 CRC64;

Query Match 91.7%; Score 33; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 3.9e-24;  
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IYINLEESQOQEKNEQELLELDKQWNLWNWF 36  
DB 81 IYINLEESQOQEKNEQELLELDKQWNLWNWF 113

RESULT 3  
Q4VUS2\_9HIV1 PRELIMINARY; PRT; 120 AA.  
AC Q4VUS2\_9HIV1 PRELIMINARY; PRT; 120 AA.  
DT 13-SEP-2005 (TREMBlrel. 31, Created)  
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN-M12;  
RA Santos A.L., Martinez A.M.B., Sassi R.M., D'Hora V., Soares E.A.J.M.,  
RA D'Avila N., Silveira J., Mendonca V.S., Leal R.G., Tanuri A.,  
RA Soares M.A.;  
RT "Determinants of HIV-1 Mother-to-Child Transmission in Southern Brazil."  
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY621387; AAW47844.1; -; Genomic\_DNA.  
KW Envelope protein.  
FT NON\_TER 1  
FT NON\_TER 120  
SQ SEQUENCE 120 AA; 14330 MW; BEF6E3214CB8D65 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 120;  
Best Local Similarity 100.0%; Pred. No. 3.6e-23;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLEESQOQEKNEQELLELDKQWNLWNWF 36  
DB 82 IYNLEESQOQEKNEQELLELDKQWNLWNWF 113

RESULT 4  
Q6WH26\_9HIV1 PRELIMINARY; PRT; 122 AA.  
AC Q6WH26\_9HIV1 PRELIMINARY; PRT; 122 AA.  
DT 05-JUL-2004 (TREMBlrel. 27, Created)  
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=14715797; DOI=10.1128/JCM.42.1.426-430.2004;  
RA Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,  
RA Gouvea M.I.F.S., Guimaraes M.A.M., De Oliveira F.E.,  
RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;  
RT "Prevalence of human immunodeficiency virus drug resistance mutations and subtypes in drug-naive, infected individuals in the army health service of Rio de Janeiro, Brazil."  
RL J. Clin. Microbiol. 42:426-430(2004).  
DR EMBL; AY285070; AAQ68133.1; -; Genomic\_RNA.  
DR SMR; Q6WH26; 1-105.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.

```
DR GO: 0005198; F-structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14758 MW; B2F2785E75F8427E CRC64;

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.6e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESONQOEKNEQELLELDKQANLWNWF 36
DB 82 IYNLLEESONQOEKNEQELLELDKQANLWNWF 113

RESULT 5
OQIWI9_9HIV1
ID Q53138_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q9QIW9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21580799; PubMed=11724274; DOI=10.1023/A:1011812810397;
RA Caride E., Hertogs K., Larder B., Dehertogh P., Brindeiro R.,
RA Machado E., de Sa C.A.M., Ever-Silva W.A., Sion F.S., Passioni L.F.C.,
RA Menezes J.A., Calazans A.R., Tanuri A.;
RT "Genotypic and phenotypic evidence of different drug-resistance
RT mutation patterns between B and non-B subtype isolates of human
RT immunodeficiency virus type 1 found in Brazilian patients failing
RT HAART.";
RL Virus Genes 23:193-202 (2001).
DR EMBL: AF165535; AAF08480.1; -; Genomic_DNA.
DR HSSP: P12488; IIMV.
DR SMR; Q9QIW9; 1-105.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0019031; C: viral envelope; IEA.
DR GO: 0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 14744 MW; 02F0BE9F79AE6C75 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 3.6e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESONQOEKNEQELLELDKQANLWNWF 36
DB 82 IYNLLEESONQOEKNEQELLELDKQANLWNWF 113

RESULT 6
Q53138_9HIV1
ID Q53138_9HIV1 PRELIMINARY; PRT; 143 AA.
AC Q53138;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=gp41;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15328081; DOI=10.1128/AAC.48.9.3253-3259.2004;
RA Menzo S., Castagna A., Monchetti A., Haseon H., Danise A., Carini E.,
RA Bagnarelli P., Lazzarin A., Clementi M.;
RT "Genotype and phenotype patterns of human immunodeficiency virus type
RT 1 resistance to enfuvirtide during long-term treatment.";
RL Antimicrob. Agents Chemother. 48:3253-3259 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Menzo S.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ964909; CAI79657.1; -; Genomic_RNA.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 143
SQ SEQUENCE 143 AA; 16814 MW; 86046F46914618F9 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 4.2e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 IYNLLEESONQOEKNEQELLELDKQANLWNWF 35
DB 112 IYNLLEESONQOEKNEQELLELDKQANLWNWF 143

RESULT 7
Q60YF3_9HIV1
ID Q60YF3_9HIV1 PRELIMINARY; PRT; 848 AA.
AC Q60YF3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstan K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Mollinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807 (2004).
DR EMBL: AY357545; AAR00902.1; -; Genomic_DNA.
DR HSSP: P04578; 1K33.
DR SMR; Q60YF3; 82-126, 194-490, 538-624.
DR GO: 0016021; C: integral to membrane; IEA.
DR GO: 0019031; C: viral envelope; IEA.
DR GO: 0005198; F: structural molecule activity; IEA.
DR InterPro: IPR000328; Env_GP41.
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 848 AA; 96698 MW; 50341627DE7FB6BA CRC64;

Query Match 88.9%; Score 32; DB 2; Length 848;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESONQOEKNEQELLELDKQANLWNWF 36
DB 640 IYNLLEESONQOEKNEQELLELDKQANLWNWF 671
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 848 AA; 96636 MW; 6077A991B48B1403 CRC64;

Query Match      88.9%; Score 32; DB 2; Length 848;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
Db 640 IYNLLEESQOQEKNEQELLELDKQWNLWNWF 671

RESULT 10
Q6UYP7_9HIV1
ID Q6UYP7_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYP7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357544; AAR00901.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYP4; 194-490, 538-624.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 848 AA; 96634 MW; CD041E0BAC44DB3B CRC64;

Query Match      88.9%; Score 32; DB 2; Length 848;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
Db 640 IYNLLEESQOQEKNEQELLELDKQWNLWNWF 671

RESULT 9
Q6UYP5_9HIV1
ID Q6UYP5_9HIV1 PRELIMINARY; PRT; 848 AA.
AC Q6UYP5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357543; AAR00900.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYP5; 194-490, 538-624.
DR GO; GO:0016021; C:integral to membrane; IEA.
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OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AV357538; AAR00897.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYP8; 1-206, 194-491, 539-625.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 849 AA; 96654 MW; DB9F480D9A9D14F9 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLEESQOQEKNEQELLELDKQANLWNWF 36
DB 641 IYNLEESQOQEKNEQELLELDKQANLWNWF 672

RESULT 12
Q6UYP3_9HIV1
ID Q6UYP3_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYP3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AV357537; AAR00896.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYP9; 194-491, 539-625.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 849 AA; 96663 MW; BCED828AB942F2E CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLEESQOQEKNEQELLELDKQANLWNWF 36
DB 641 IYNLEESQOQEKNEQELLELDKQANLWNWF 672

RESULT 13
Q6UYQ3_9HIV1
ID Q6UYQ3_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYQ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357533; AAR00892.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYQ3; 1-217, 194-490, 535-624.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 849 AA; 96637 MW; A30D2A6F412F19A9 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLEESQOQEKNEQELLELDKQANLWNWF 36
DB 640 IYNLEESQOQEKNEQELLELDKQANLWNWF 671

RESULT 14
Q6UYQ5_9HIV1
ID Q6UYQ5_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYQ5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14990699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AV357537; AAR00896.1; -; Genomic_DNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6UYP9; 194-491, 539-625.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:vital envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON TER 1
SQ SEQUENCE 849 AA; 96663 MW; BCED828AB942F2E CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLEESQOQEKNEQELLELDKQANLWNWF 36
DB 640 IYNLEESQOQEKNEQELLELDKQANLWNWF 671
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RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357530; AAR00890.1; -; Genomic_DNA.
DR HSSP; P04578; IK33.
DR SMR; Q6UYQ5; 194-490, 535-624.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF0516; GP120; 1.
DR Pfam; PF0517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 849 AA; 96667 MW; CED40F4AE1574B58 CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQEKNEQELLELDKQANLWNWF 36
Db 640 IYNLLEESQOQEKNEQELLELDKQANLWNWF 671

RESULT 15
Q6UYQ6_9HIV1
ID Q6UYQ6_9HIV1 PRELIMINARY; PRT; 849 AA.
AC Q6UYQ6_
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14950699; DOI=10.1128/JVI.78.6.2790-2807.2004;
RA Kuhnmann S.E., Pugach P., Kunstman K.J., Taylor J., Stanfield R.L.,
RA Snyder A., Strizki J.M., Riley J., Baroudy B.M., Wilson I.A.,
RA Korber B.T., Wolinsky S.M., Moore J.P.;
RT "Genetic and phenotypic analyses of human immunodeficiency virus type
RT 1 escape from a small-molecule CCR5 inhibitor.";
RL J. Virol. 78:2790-2807(2004).
DR EMBL; AY357529; AAR00889.1; -; Genomic_DNA.
DR HSSP; P04578; IK33.
DR SMR; Q6UYQ6; 194-490, 538-624.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF0516; GP120; 1.
DR Pfam; PF0517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
FT NON_TER 1
SQ SEQUENCE 849 AA; 96782 MW; 8061276D3343029A CRC64;

Query Match 88.9%; Score 32; DB 2; Length 849;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYNLLEESQOQEKNEQELLELDKQANLWNWF 36
Db 640 IYNLLEESQOQEKNEQELLELDKQANLWNWF 671
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Search completed: March 6, 2006, 16:25:17  
Job time : 123 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:25:38 ; Search time 28.6667 Seconds  
(without alignments)  
103.825 Million cell updates/sec

Title: US-09-809-060A-3  
Perfect score: 36  
Sequence: 1 YTGIIYNLEESQOQKNEQELLELDKWNLNWVF 36

Scoring table:  
OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/H COMB.pap.\*  
4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap.\*  
5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap.\*  
6: /cgn2\_6/ptodata/1/iaa/backfile1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	36	100.0	36	2	US-08-484-223B-4
5	36	100.0	36	2	US-08-919-597-4
6	36	100.0	36	2	US-08-475-668A-4
7	36	100.0	36	2	US-08-485-551A-4
8	36	100.0	36	2	US-08-471-913A-4
9	36	100.0	36	2	US-08-554-616-4
10	36	100.0	36	2	US-08-485-264A-4
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17	36	100.0	36	2	US-08-973-952-4
18	36	100.0	36	2	US-08-470-896-4
19	36	100.0	36	2	US-08-485-546A-4
20	36	100.0	36	2	US-09-834-784-1358
21	36	100.0	36	2	US-09-834-784-1359
22	36	100.0	36	2	US-09-515-965A-1358
23	36	100.0	36	2	US-09-515-965A-1359
24	36	100.0	36	2	US-09-350-641C-1358
25	36	100.0	36	2	US-09-350-641C-1359
26	36	100.0	36	2	US-09-350-841A-1358
27	36	100.0	36	2	US-09-350-841A-1359

28 36 100.0 36 2 US-08-487-266A-4 Sequence 4, Appli  
29 36 100.0 36 2 US-09-623-548A-1422 Sequence 1422, Ap  
30 36 100.0 36 2 US-10-252-136-4 Sequence 4, Appli  
31 36 100.0 36 2 US-09-657-276-1422 Sequence 1422, Ap  
32 36 100.0 36 2 US-08-484-741-4 Sequence 4, Appli  
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34 36 100.0 269 2 US-08-965-056-33 Sequence 33, Appli  
35 36 100.0 865 2 US-07-956-483-13 Sequence 13, Appli  
36 36 100.0 887 2 US-08-472-240A-4 Sequence 4, Appli  
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38 26 72.2 36 2 US-08-360-107A-3 Sequence 3, Appli  
39 26 72.2 36 2 US-08-554-616-3 Sequence 3, Appli  
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## ALIGNMENTS

RESULT 1  
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; Sequence 4, Application US/08073028  
; Patent No. 5464933  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
; TITLE OF INVENTION: TRANSMISSION  
; NUMBER OF SEQUENCES: 74  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edwards  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/073,028  
; FILING DATE: 07-JUN-1993  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-004-999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-073-028-4

Query Match 100.0%; Score 36; DB 1; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLEESQOQKNEQELLELDKWNLNWVF 36  
|||||

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

## RESULT 2

US-08-486-099-4  
; Sequence 4, Application US/08486099  
; Patent No. 6013263  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
; TITLE OF INVENTION: B VIRUS TRANSMISSION  
; NUMBER OF SEQUENCES: 209  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/486,099  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-031  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-486-099-4

Query Match 100.0%; Score 36; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-27; Mismatches 0; Indels 0; Gaps 0;

Matches 36; Conservative 0;

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

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Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

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Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

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Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

Db 1 YTGIIYNLLEESQKNEQELLELDKQWNLWNWF 36

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484,223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-484-223B-4

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36  
|||||  
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

## RESULT 5

US-08-919-597-4  
Sequence 4, Application US/08919597  
Patent No. 6054265  
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION  
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 273  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/919,597  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/470,896  
FILING DATE: 06-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-020  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-919-597-4

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36  
|||||  
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

## RESULT 6

US-08-475-668A-4  
Sequence 4, Application US/08475668A  
Patent No. 6060065  
GENERAL INFORMATION:

APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 211  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: PC-DOS/MS-DOS  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/475,668A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-026  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-475-668A-4

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36  
|||||  
DB 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

```
RESULT 7
US-08-485-551A-4
; Sequence 4, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-485-551A-4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. NO. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 8
US-08-471-913A-4
; Sequence 4, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
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```
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-471-913A-4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. NO. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36
Db 1 YTGIIYNLLEESQNOQEKNEQELLELDKQWNLWNWF 36

RESULT 9
US-08-554-616-4
; Sequence 4, Application US/08554616
; Patent No. 6133418
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/554,616
; FILING DATE: 06-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; APPLICATION NUMBER: US 08/073,028
; FILING DATE: 07-JUN-1993
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-554-616--4

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 11
US-09-082-279B-1358
; Sequence 1358, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1358
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-1358

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

RESULT 12
US-09-082-279B-1359
; Sequence 1359, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; FILE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1359
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-082-279B-1359

Query Match 100.0%; Score 36; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
DB 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36
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QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36  
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

## RESULT 13

US-08-474-349A-4  
; Sequence 4, Application US/08474349A  
; Patent No. 6333395  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE  
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA  
; TITLE OF INVENTION: VIRUS TRANSMISSION  
; NUMBER OF SEQUENCES: 517  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,349A  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-024  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-474-349A-4

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36  
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

## RESULT 14

US-09-315-304B-1358  
; Sequence 1358, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S. K.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.

; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1358  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1358

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36  
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

## RESULT 15

US-09-315-304B-1359  
; Sequence 1359, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S. K.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; CURRENT FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1359  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1359

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-27;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36  
Db 1 YTGIIYNLLEESQOQEKNEQELLELDKQWNLWNWF 36

Search completed: March 6, 2006, 16:27:50  
Job time : 28.6667 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 16:26:33 ; Search time 97.3333 Seconds  
(without alignments)  
154.540 Million cell updates/sec

Title: US-09-809-060A-3  
Perfect score: 36  
Sequence: 1 YTGIIYNLLSESQNQKNEQELLELDKQWNLWNWF 36

Scoring table: OLIGO  
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Searched: 1867569 seqs, 417829326 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	36	100.0	36	4	US-10-252-136-4
3	36	100.0	36	4	US-10-351-641-1358
4	36	100.0	36	4	US-10-351-641-1359
5	36	100.0	36	4	US-10-267-682-4
6	36	100.0	36	4	US-10-267-748-4
7	36	100.0	36	4	US-10-663-589-39
8	36	100.0	36	4	US-10-671-282-39
9	36	100.0	36	5	US-10-168-295-4
10	36	100.0	36	5	US-10-950-010-4
11	36	100.0	36	6	US-11-066-697-1422
12	36	100.0	269	3	US-09-854-816-33
13	26	72.2	38	4	US-10-086-409A-3
14	26	72.2	45	4	US-10-086-409A-6
15	23	63.9	36	3	US-09-809-060-2
16	23	63.9	36	4	US-10-252-136-3
17	23	63.9	36	4	US-10-351-641-856
18	23	63.9	36	4	US-10-351-641-1051
19	23	63.9	36	4	US-10-351-641-1357
20	23	63.9	36	4	US-10-267-682-3
21	23	63.9	36	4	US-10-267-748-3
22	23	63.9	36	4	US-10-663-589-38
23	23	63.9	36	4	US-10-671-282-38
24	23	63.9	36	5	US-10-168-295-3
25	23	63.9	36	5	US-10-950-010-3
26	23	63.9	36	5	US-10-950-010-541
27	23	63.9	36	6	US-11-066-697-1421

28 23 63.9 70 6 US-11-018-102-13 Sequence 13, Appl  
29 23 63.9 145 3 US-09-131-551-11 Sequence 11, Appl  
30 23 63.9 145 4 US-10-000-321-11 Sequence 11, Appl  
31 23 63.9 269 3 US-09-854-816-28 Sequence 28, Appl  
32 23 63.9 269 3 US-09-854-816-30 Sequence 30, Appl  
33 23 63.9 269 3 US-09-854-816-31 Sequence 31, Appl  
34 23 63.9 285 6 US-11-018-102-11 Sequence 11, Appl  
35 21 58.3 21 4 US-10-351-641-1082 Sequence 1082, Ap  
36 21 58.3 21 4 US-10-351-641-1083 Sequence 1083, Ap  
37 21 58.3 27 4 US-10-005-305-58 Sequence 58, Appl  
38 21 58.3 27 4 US-10-005-305-73 Sequence 73, Appl  
39 21 58.3 27 5 US-10-950-010-125 Sequence 125, App  
40 21 58.3 28 4 US-10-005-305-59 Sequence 59, Appl  
41 21 58.3 28 4 US-10-005-305-72 Sequence 72, Appl  
42 21 58.3 28 5 US-10-950-010-124 Sequence 124, App  
43 21 58.3 29 4 US-10-351-641-635 Sequence 635, App  
44 21 58.3 29 4 US-10-351-641-637 Sequence 637, App  
45 21 58.3 29 4 US-10-005-305-60 Sequence 60, Appl

## ALIGNMENTS

RESULT 1  
US-09-809-060-3  
; Sequence 3, Application US/09809060  
; Publication No. US20020010317A1  
; GENERAL INFORMATION:  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Allaway, Graham P.  
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit  
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active  
; TITLE OF INVENTION: Regions of HIV Envelope Proteins  
; FILE REFERENCE: 1900.0260001  
; CURRENT APPLICATION NUMBER: US/09/809, 060  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: US 60/189,981  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-809-060-3

Query Match 100.0%; Score 36; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 96-28; 0; Gaps 0;  
Matches 36; Conservative 0; Mismatches 0; Indels 0;  
QY 1 YTGIIYNLLSESQNQKNEQELLELDKQWNLWNWF 36  
DB 1 YTGIIYNLLSESQNQKNEQELLELDKQWNLWNWF 36

RESULT 2  
US-10-252-136-4  
; Sequence 4, Application US/10252136  
; Publication No. US20030103998A1  
; GENERAL INFORMATION:  
; APPLICANT: Johnson, M. Ross  
; APPLICANT: Lambert, Dennis M.  
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER  
; TITLE OF INVENTION: VIRAL INFECTIONS  
; TITLE OF INVENTION: USING COMBINATORY THERAPY  
; FILE REFERENCE: 7872-036  
; CURRENT APPLICATION NUMBER: US/10/252,136  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: US/08/973,952  
; PRIOR FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 82  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4



Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 9e-28;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36  
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 6  
US-10-267-748-4  
; Sequence 4, Application US/10267748  
; Publication No. US20040052820A1  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; Matthews, Thomas J.  
; Wild, Carl T.  
; Barney, Shawn O.  
; Lambert, Dennis M.  
; Petteway, Stephen R.  
; Langlois, Alphonse J.  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION  
; NUMBER OF SEQUENCES: 239  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/267,748  
; FILING DATE: 08-Oct-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,223A  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Cortuzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-029  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-267-748-4

Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 9e-28;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36  
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 7

US-10-663-589-39  
; Sequence 39, Application US/10663589  
; Publication No. US20040063637A1  
; GENERAL INFORMATION:  
; APPLICANT: Trimeris, Inc.  
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV  
; FILE REFERENCE: TRM-003  
; CURRENT APPLICATION NUMBER: US/10/663,589  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: US 60/414,441  
; PRIOR FILING DATE: 2002-09-27  
; NUMBER OF SEQ ID NOS: 95  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 39  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthesized  
; US-10-663-589-39

Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 9e-28;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36  
Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 8  
US-10-671-282-39  
; Sequence 39, Application US/10671282  
; Publication No. US20040122214A1  
; GENERAL INFORMATION:  
; APPLICANT: Trimeris, Inc.  
; TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and  
; FILE REFERENCE: TRM-004  
; CURRENT APPLICATION NUMBER: US/10/671,282  
; CURRENT FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: 60/414,439  
; PRIOR FILING DATE: 2002-09-27  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 39  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: synthesized  
; US-10-671-282-39

Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 9e-28;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YTGIIYNLLEESQKQKNEQELLELDKQWNLWNWF 36

RESULT 9  
US-10-168-295-4  
; Sequence 4, Application US/10168295  
; Publication No. US20050065319A1  
; GENERAL INFORMATION:  
; APPLICANT: Baroudy, Bahige M.  
; TITLE OF INVENTION: Combination Method For Treating Viral Infections  
; FILE REFERENCE: IN01358  
; CURRENT APPLICATION NUMBER: US/10/168,295  
; CURRENT FILING DATE: 2002-06-19

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; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PR
; ORGANISM: Human immunodeficiency virus t
US-10-168-295-4

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Query Match	100.0%;	Score 36;	DB 5;	Length 36;
Best Local Similarity	100.0%;	Pred. No. 9e-28;		
Matches 36;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;				

Qy 1 YTGIIYNLEESNQQRKEQELJELDKWANLWNWF 36

Db 1 YTGIIYNLEESNQQRKEQELJELDKWANLWNWF 36

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RESULT 10
US-10-950-010-4
; Sequence 4, Application US/10950010
; Publication No. US20050070475A1
; GENERAL INFORMATION:
; APPLICANT: BRIDON, Dominique P.
; APPLICANT: DUPRESNE, Robert S.
; APPLICANT: BOUDJELLAB, Nissab
; APPLICANT: ROBITAILLE, Martin
; APPLICANT: MILNER, Peter G.
; TITLE OF INVENTION: LONG LASTING FUSION PEPTIDE INHIBITORS OF VIRAL
; TITLE OF INVENTION: INFECTION
; FILE REFERENCE: 500862001501/REDC-1512
; CURRENT APPLICATION NUMBER: US/10/950,010
; CURRENT FILING DATE: 2004-09-24
; PRIOR APPLICATION NUMBER: US 09/623,533
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: PCT/US00/13651
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: US 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/153,406
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-950-010-4

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Query Match      100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 9e-28;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 11  
US-11-066-697-1422  
; Sequence 1422, Application US/11066697  
; Publication No. US20050187159A1  
; GENERAL INFORMATION:  
; APPLICANT: Bridon, Dominique P.  
; APPLICANT: Ezrin, Alan M.  
; APPLICANT: Milner, Peter G.  
; APPLICANT: Holmes, Warren L.  
;

```

/ APPLICANT: Thibaudeau, Karen
/ TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
/ TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
/ TITLE OF INVENTION: COMPONENTS
/ FILE REFERENCE: 500862002301
/ CURRENT APPLICATION NUMBER: US/11/0666,697
/ CURRENT FILING DATE: 2005-02-25
/ PRIOR APPLICATION NUMBER: 09/657,276
/ PRIOR FILING DATE: 2000-09-07
/ PRIOR APPLICATION NUMBER: 60/153,406
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: 60/159,783
/ PRIOR FILING DATE: 1999-10-15
/ NUMBER OF SEQ ID NOS: 1617
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1422
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Peptide
US-11-066-697-1422

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Query Match	100.0%	Score 36;	DB 6;	Length 36;
Best Local Similarity	100.0%	Pred. No. 9e-28;		
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Db 1 YTGIIYNLLEESQOQKEQELLELDKWANLWNWF 36

RESULT 12  
US-09-854-816-33  
Sequence 33, Application US/09854816  
Patent No. US20020151473A1  
GENERAL INFORMATION:  
APPLICANT: Andrew C. Braisted  
J. Kevin Judice  
Robert S. McDowell  
J. Christopher Phelan  
Melissa A. Starovasnik  
James A. Wells  
TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
Making Same  
NUMBER OF SEQUENCES: 113  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/854,816  
FILING DATE: 15-May-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/965,056  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Torchia, PhD., Timothy E.  
REGISTRATION NUMBER: 36,700  
REFERENCE/DOCKET NUMBER: PL005R2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-8674  
TELEFAX: 650/952-9881

Qy 8 LLESONQKEKNEQELLELDKWA 30

QY 8 LLEESQOQKEKNEQELLELDKWA 30

Db 8 LLEESQOQEKNEQELLELDKWA 30

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Job time : 97.3333 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:28:08 ; Search time 10.3333 Seconds  
(without alignments)  
69.679 Million cell updates/sec

Title: US-09-809-060A-3  
Perfect score: 36  
Sequence: 1 YTGIIYNLLSESQKQKNEQELLELDKWNLWHP 36

Scoring table: OLIGO  
Gapop 60.0 , Capext 60.0

Searched: 135346 seqs, 20000420 residues

Word size : 0

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0  
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	21	58.3	36	6	US-10-841-956A-1
3	21	58.3	36	7	US-11-029-003-1
4	21	58.3	36	7	US-11-187-687-22
5	21	58.3	37	7	US-11-112-277-33
6	21	58.3	44	7	US-11-089-426-10
7	21	58.3	44	7	US-11-187-687-24
8	21	58.3	267	6	US-10-841-956A-4
9	21	58.3	269	6	US-10-841-956A-8
10	21	58.3	270	6	US-10-841-956A-5
11	21	58.3	281	6	US-10-841-956A-7
12	21	58.3	282	6	US-10-841-956A-6
13	21	58.3	293	6	US-10-841-956A-9
14	21	58.3	354	7	US-11-053-100-27
15	21	58.3	356	7	US-11-053-100-36
16	21	58.3	357	7	US-11-053-100-30
17	21	58.3	357	7	US-11-053-100-33
18	21	58.3	504	7	US-11-053-100-28
19	21	58.3	506	7	US-11-053-100-37
20	21	58.3	507	7	US-11-053-100-31
21	21	58.3	507	7	US-11-053-100-34
22	21	58.3	654	7	US-11-053-100-29
23	21	58.3	656	7	US-11-053-100-38
24	21	58.3	657	7	US-11-053-100-32
25	21	58.3	657	7	US-11-053-100-35

RESULT 1  
US-11-084-858-11  
; Sequence 11, Application US/11084858  
; Publication No. US20050271678A1  
; GENERAL INFORMATION:  
; APPLICANT: BRUST, Stefan  
; KNAPP, Stefan  
; GERKEN, Manfred  
; GUERTLER, Lutz  
; TITLE OF INVENTION: Peptides derived from a retrovirus of the HIV group, and their use  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/084,858  
; FILING DATE: 21-Mar-2005  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/10/000,321  
; FILING DATE: 04-Dec-2001  
; APPLICATION NUMBER: 09/131,551  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANDERCOCK, Colin G.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 58315/106/BEAK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 145 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

#### ALIGNMENTS

Sequence 8, Appl  
Sequence 13, Appl  
Sequence 1, Appl  
Sequence 5, Appl  
Sequence 1, Appl  
Sequence 3, Appl  
Sequence 4, Appl  
Sequence 9, Appl  
Sequence 19, Appl  
Sequence 1, Appl  
Sequence 7, Appl  
Sequence 9, Appl  
Sequence 2, Appl  
Sequence 6, Appl  
Sequence 36, Appl  
Sequence 38, Appl  
Sequence 10, Appl  
Sequence 12, Appl

## US-11-084-858-11

Query Match 63.9%; Score 23; DB 7; Length 145;  
Best Local Similarity 100.0%; Pred. No. 9.6e-17;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 LLEESQKQKNEQELLELDKWA 30  
|||||  
DB 113 LLEESQKQKNEQELLELDKWA 135

## RESULT 2

US-10-841-956A-1  
; Sequence 1, Application US/10841956A  
; Publication No. US20050281829A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN HEHIR, CRISTINA A.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: STATTEL, JAMES M.  
; APPLICANT: PALOMBELLA, VITO J.  
; APPLICANT: BITONTI, ALAN R.  
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS  
; FILE REFERENCE: 08945.0003-00000  
; CURRENT APPLICATION NUMBER: US/10/841,956A  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: 60/468,835  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-841-956A-1

Query Match 58.3%; Score 21; DB 6; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKQKNEQELLELDKWA 30  
|||||  
DB 10 EESQKQKNEQELLELDKWA 30

## RESULT 3

US-11-029-003-1  
; Sequence 1, Application US/11029003  
; Publication No. US20050260194A1  
; GENERAL INFORMATION:  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: RIVERA, DANIEL S.  
; APPLICANT: BITONTI, ALAN J.  
; APPLICANT: STATTEL, JAMES  
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS  
; FILE REFERENCE: 08945.0007-01000  
; CURRENT APPLICATION NUMBER: US/11/029,003  
; CURRENT FILING DATE: 2005-01-05  
; PRIOR APPLICATION NUMBER: 60/539,207  
; PRIOR FILING DATE: 2004-01-26  
; PRIOR APPLICATION NUMBER: 60/487,964  
; PRIOR FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: 60/469,600  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-11-029-003-1

Query Match 58.3%; Score 21; DB 7; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKQKNEQELLELDKWA 30  
|||||  
DB 10 EESQKQKNEQELLELDKWA 30

## RESULT 4

US-11-187-687-22  
; Sequence 22, Application US/11187687  
; Publication No. US20060019347A1  
; GENERAL INFORMATION:  
; APPLICANT: Cho, Ho Sung  
; APPLICANT: Daniel, Thomas O.  
; APPLICANT: Hays, Anna-Maria  
; APPLICANT: Wilson, Troy E.  
; APPLICANT: Litzinger, David C.  
; APPLICANT: Mariani, Roberto  
; APPLICANT: Kimmel, Bruce E.  
; APPLICANT: Keefe, William M.  
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino  
; FILE REFERENCE: AMEX-0041.00US  
; CURRENT APPLICATION NUMBER: US/11/187,687  
; CURRENT FILING DATE: 2005-07-21  
; PRIOR APPLICATION NUMBER: 60/590,035  
; PRIOR FILING DATE: 2004-07-21  
; PRIOR APPLICATION NUMBER: 60/659,709  
; PRIOR FILING DATE: 2005-03-07  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 22  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-11-187-687-22

Query Match 58.3%; Score 21; DB 7; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQKQKNEQELLELDKWA 30  
|||||  
DB 10 EESQKQKNEQELLELDKWA 30

## RESULT 5

US-11-112-277-33  
; Sequence 33, Application US/11112277  
; Publication No. US20050267293A1  
; GENERAL INFORMATION:  
; APPLICANT: Bousquet-Gagnon, Nathalie  
; APPLICANT: Quraishi, Omar  
; APPLICANT: Bridon, Dominique P.  
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN  
; FILE REFERENCE: 500862003700  
; CURRENT APPLICATION NUMBER: US/11/112,277  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/565,228  
; PRIOR FILING DATE: 2004-04-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 37  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: T20 Analogue  
; FEATURE:  
; NAME/KEY: MOD\_RES



```
; LOCATION: 37
; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-33

Query Match      58.3%; Score 21; DB 7; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.8e-15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30
   |||||
Db 10 EESQOQEKNEQELLELDKWA 30

RESULT 6
US-11-089-426-10
; Sequence 10, Application US/11089426
; Publication No. US20050261229A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: Fc Fusion Proteins For Enhancing the Immunogenicity of
; FILE REFERENCE: LEX-007
; CURRENT APPLICATION NUMBER: US/11/089,426
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US/09/621,268
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/144,965
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fused
; OTHER INFORMATION: polypeptide from pDC-muFC vector
US-11-089-426-10

Query Match      58.3%; Score 21; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.3e-15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30
   |||||
Db 8 EESQOQEKNEQELLELDKWA 28

RESULT 7
US-11-187-687-24
; Sequence 24, Application US/11187687
; Publication No. US20060019347A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Ho Sung
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Hays, Anna-Maria
; APPLICANT: Wilson, Troy E.
; APPLICANT: Litzinger, David C.
; APPLICANT: Mariani, Roberto
; APPLICANT: Kimmel, Bruce E.
; APPLICANT: Keefe, William M.
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
; FILE REFERENCE: AMBX-0041.00US
; CURRENT APPLICATION NUMBER: US/11/187,687
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: 60/590,035
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: 60/659,709
; PRIOR FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 28
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; SOFTWARE: Patentin version 3.3
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-24

Query Match      58.3%; Score 21; DB 7; Length 44;
Best Local Similarity 100.0%; Pred. No. 3.3e-15;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30
   |||||
Db 18 EESQOQEKNEQELLELDKWA 38

RESULT 8
US-10-841-956A-4
; Sequence 4, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 4
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Construct
US-10-841-956A-4

Query Match      58.3%; Score 21; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 EESQOQEKNEQELLELDKWA 30
   |||||
Db 241 EESQOQEKNEQELLELDKWA 261

RESULT 9
US-10-841-956A-8
; Sequence 8, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 8
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:31:26 ; Search time 114.667 Seconds  
(without alignments)  
137.945 Million cell updates/sec

Title: US-09-809-060A-4  
Perfect score: 192  
Sequence: 1 YTSLLVSLLEKSIQEQKNEQLLELDKWSLWNP 36

Scoring table: BLOSUM62

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 1130394

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq\_21.\*

1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	100.0	36	3 AAY89840	Aay89840 Core poly
2	192	100.0	36	3 AAY89841	Aay89841 Core poly
3	192	100.0	36	4 AAB78242	Aab78242 Core poly
4	192	100.0	36	4 AAB78241	Aab78241 Core poly
5	192	100.0	36	4 AAU70182	Aau70182 HIV viral
6	192	100.0	36	4 ABB01248	Abb01248 Viral DP1
7	192	100.0	36	4 ABB01249	Abb01249 Viral DP1
8	192	100.0	36	4 ABB02833	Abb02833 Viral cor
9	192	100.0	36	4 AAU13794	Aau13794 DP178-lik
10	192	100.0	36	4 AAU13795	Aau13795 DP178-lik
11	192	100.0	36	5 AAO18774	Aao18774 HIV gp41
12	192	100.0	36	5 AAO18826	Aao18826 HIV gp41
13	192	100.0	36	5 ADE02854	Ade02854 Hybrid po
14	192	100.0	36	5 ADE02853	Ade02853 Hybrid po
15	192	100.0	36	8 ADN06925	Adn06925 Peptide #
16	192	100.0	36	8 ADS87260	Ads87260 HIV-1 gp4
17	192	100.0	36	9 ADY71547	Ady71547 HIV-1 tra
18	192	100.0	36	9 ABB071495	Abb071495 HIV-1 tra
19	189	98.4	36	4 ABB02834	Abb02834 Viral cor
20	187	97.4	36	2 AAR98401	Aar98401 Peptide c
21	187	97.4	36	2 AAU17014	Aau17014 DP-178-lik
22	187	97.4	36	4 AAB54788	Aab54788 HIV antiv
23	187	97.4	36	4 AAB92247	Aab92247 Virus res
24	187	97.4	36	4 AAG67042	Aag67042 HIV-1 gp4

#### ALIGNMENTS

##### RESULT 1

AAy89840  
ID AAY89840 standard; peptide; 36 AA.  
XX  
AC AAY89840;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Core polypeptide fragment T No. 1409.  
XX  
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.  
XX  
OS Unidentified.  
XX  
FN WO9959615-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US011219.  
XX  
PR 20-MAY-1998; 98US-00082279.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
WPI; 2000-136792/12.

A new hybrid polypeptide with enhanced pharmacokinetic properties comprises enhancer sequence.

Disclosure; Page 45; 124pp; English.

The invention relates to hybrid polypeptides comprising enhancer peptide sequence linked to core polypeptides. The enhancer polypeptides are derived from various retroviral envelope (gp41) protein sequences, especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the pharmacokinetic properties such as increasing the half-life of any core polypeptide that they are linked to. The core polypeptides are any polypeptide that may be introduced into a living system and that can function as a pharmacologically useful peptide for the treatment or prevention of a disease. The core polypeptides are bioactive peptides selected from a growth factor, cytokine, differentiation factor, interleukin, interferon, colony stimulating factor, hormone or angiogenic



RESULT 4  
 AAB78241 ID AAB78241 standard; peptide; 36 AA.  
 XX AC  
 XX AC AAB78241;  
 XX DT 19-APR-2001 (first entry)  
 XX DE Core polypeptide T1409.  
 XX DE Core polypeptide; enhancer; antiviral; anti-HIV; virucide; hepatotropic;  
 XX KW antiinflammatory; hybrid polypeptide; coiled-coil peptide interaction;  
 XX KW fusion-related disorder; bacterial infection; viral infection.  
 XX OS Unidentified.  
 XX PN WO200103723-A1.  
 XX PD 18-JAN-2001.  
 XX PF 10-JUL-2000; 2000WO-US018772.  
 XX PR 09-JUL-1999; 99US-00350641.  
 XX PA (TRIM-) TRIMERIS INC.  
 XX PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
 XX DR WPI; 2001-147136/15.  
 XX PT New hybrid polypeptide, useful for preventing, treating and diagnosing  
 XX PT e.g. viral infections, comprises an enhancer peptide linked to a core  
 XX PT polypeptide.  
 XX PS Disclosure; Page 58; 151pp; English.  
 XX CC The present sequence is a core polypeptide which may be linked to an  
 CC enhancer peptide to form a novel hybrid polypeptide. The hybrid  
 CC polypeptide exhibits enhanced pharmacokinetic properties relative to  
 CC those exhibited by the core polypeptide when introduced into a living  
 CC system. It is used to increase the in vitro or ex vivo half-life of the  
 CC core polypeptide. The hybrid and core polypeptides can be used for  
 CC modulating fusogenic events and intracellular processes involving coiled-  
 CC coil peptide interactions. Other uses include preventing, treating and/or  
 CC diagnosing disorders involving fusion events (e.g. modulation of  
 CC neurotransmitter exchange and sperm-egg fusion), intracellular processes  
 CC involving coiled-coil peptides (e.g. bacterial infections) and viral  
 CC infections that involve cell-cell and/or virus-cell fusion (e.g. viral  
 CC infections caused by human immunodeficiency virus, respiratory syncytial  
 CC virus, Epstein-Barr virus, hepatitis B virus, Mason-Pfizer virus and  
 CC polio virus). The enhancer peptide sequence increases the half-life and  
 CC reduces the clearance rate of therapeutic peptides, which increases their  
 CC efficacy and minimises the incidence and severity of adverse side  
 CC effects. In addition, this increases the sensitivity of the diagnostic  
 CC procedure in which they are used  
 XX SQ Sequence 36 AA;  
 Query Match 100.0%; Score 192; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSLIYSLLEKSQIQQKNEQELLELDKQWASLWNWF 36  
 Db 1 YTSLIYSLLEKSQIQQKNEQELLELDKQWASLWNWF 36  
 RESULT 5  
 AAU70182 ID AAU70182 standard; peptide; 36 AA.  
 XX AC  
 XX AC AAU70182;  
 XX DT 14-FEB-2002 (first entry)  
 XX DE HIV viral envelope protein stabilising peptide #4.  
 XX KW Human; HIV-1; human immunodeficiency virus; gp41; glycoprotein 41; gp120;  
 XX KW anti-HIV; stabilising peptide; viral envelope protein; glycoprotein 120;  
 XX KW alpha-helical region; ectodomain.  
 XX OS Homo sapiens.  
 XX PN WO200170262-A2.  
 XX PD 27-SEP-2001.  
 XX PF 15-MAR-2001; 2001WO-US008108.  
 XX PR 17-MAR-2000; 2000US-0189981P.  
 XX PA (PANA-) PANACOS PHARM INC.  
 XX PI Wild CT, Allaway GP;  
 XX DR WPI; 2001-626098/72.  
 XX PT Immunogenic composition for inhibiting HIV infection, comprises viral  
 XX PT envelope protein or its fragment exterior to viral membrane, a  
 XX PT stabilizing peptide, and, optionally, viral cell surface receptor or its  
 XX PT fragment.  
 XX PS Claim 6; Page 45; 84pp; English.  
 XX CC The invention relates to methods of generating immunogens that elicit  
 CC neutralising antibodies which target regions of viral envelope proteins  
 CC such as the gp120/gp41 (glycoprotein 120/glycoprotein 41) complex of HIV-  
 CC 1 (human immunodeficiency virus 1). Sequences AAU70179-AAU70198 and  
 CC AAU70677-AAU70743 represent stabilising peptides modelling the alpha-  
 CC helical regions of the ectodomain of the HIV-1 transmembrane protein to  
 CC stabilise fusion-active intermediate structures, which can be used as  
 CC vaccine immunogens. Immunogenic compositions comprise a viral envelope  
 CC protein or its fragment exterior to the viral membrane, a stabilising  
 CC peptide to disrupt formation of structural intermediates necessary for  
 CC viral fusion and entry, and optionally, a viral cell surface receptor or  
 CC its fragment. The stabilising peptide is capable of associating with the  
 CC envelope protein or its fragment to form a stabilised, fusion active  
 CC structure. Antibody binding assays are used to determine the ability of  
 CC immunogen vaccines to generate an immune response to various forms of  
 CC envelope. Virus neutralisation assays can be used to characterise the  
 CC antibody response raised against HIV-1 gp41 domains. The sequences and  
 CC methods are useful for inhibiting HIV infection, for inducing an immune  
 CC response in an animal and for raising antibodies  
 XX SQ Sequence 36 AA;  
 Query Match 100.0%; Score 192; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSLIYSLLEKSQIQQKNEQELLELDKQWASLWNWF 36  
 Db 1 YTSLIYSLLEKSQIQQKNEQELLELDKQWASLWNWF 36  
 RESULT 6  
 ABB01248 ID ABB01248 standard; peptide; 36 AA.  
 XX AC  
 XX AC ABB01248;  
 XX DT 11-SEP-2003 (revised)  
 XX DT 06-AUG-2003 (revised)  
 XX DT 03-JAN-2002 (first entry)







CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to  
 CC amino acids 639-673 of the transmembrane protein gp41 from human  
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
 CC also relates to a method of identifying compounds that inhibit the  
 CC formation of or disruption of a DP107/DP178 complex. The method comprises  
 CC detecting the formation of a DP107/DP178 complex, both in the presence or  
 CC absence of a test compound, in a reaction mixture containing DP107 and  
 CC DP178 peptides. The method is useful for identifying compounds, including  
 CC small molecule compounds, which may themselves exhibit antifusogenic,  
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like  
 CC peptides are useful to inhibit human and non-human retroviral,  
 CC particularly HIV, transmission to uninfected cells. The present sequence  
 CC represents one of the DP178-like/DP107-like peptides of the invention  
 XX  
 XX Sequence 36 AA;

Query Match 100.0%; Score 192; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36  
 |||||  
 Db 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

## RESULT 11

AAO18774  
 ID AAO18774 standard; peptide; 36 AA.

XX AAO18774;

XX DT 29-OCT-2002 (first entry)

XX DE HIV gp41 protein DP-178 region derived peptide SEQ ID NO: 5.

XX KW Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;  
 XX gp41.

XX OS Human immunodeficiency virus.

XX PN WO200256902-A2.

XX PD 25-JUL-2002.

XX PF 17-DEC-2001; 2001WO-US048802.

XX PR 19-DEC-2000; 2000US-0256657P.

XX PA (SCHE ) SCHERING CORP.

XX PI Baroudy BM;

XX DR WPI; 2002-636513/68.

XX PT Treatment of HIV infection in an individual involves administration of a  
 XX combination of chemokine co-receptor five antagonist and a specified HIV  
 XX envelope polypeptide.

XX PS Disclosure; Page 32; 52pp; English.

XX CC The present invention relates to a method of treating an HIV infection in  
 XX an individual, which involves administering in combination a chemokine co  
 XX -receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its  
 XX derivative. Other viral infections can also be treated using the method.  
 XX The present sequence is a peptide derived from HIV and useful in the  
 XX method of the invention

XX Sequence 36 AA;

Query Match 100.0%; Score 192; DB 5; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-16;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36  
 |||||  
 Db 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

## RESULT 12

AAO18826  
 ID AAO18826 standard; peptide; 36 AA.

XX AAO18826;

XX DT 29-OCT-2002 (first entry)

XX DE HIV gp41 protein DP-178 region derived peptide SEQ ID NO: 57.

XX KW Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;  
 XX gp41.

XX OS Human immunodeficiency virus.

XX PN WO200256902-A2.

XX PD 25-JUL-2002.

XX PF 17-DEC-2001; 2001WO-US048802.

XX PR 19-DEC-2000; 2000US-0256657P.

XX PA (SCHE ) SCHERING CORP.

XX PI Baroudy BM;

XX DR WPI; 2002-636513/68.

XX PT Treatment of HIV infection in an individual involves administration of a  
 XX combination of chemokine co-receptor five antagonist and a specified HIV  
 XX envelope polypeptide.

XX PS Disclosure; Page 34; 52pp; English.

XX CC The present invention relates to a method of treating an HIV infection in  
 XX an individual, which involves administering in combination a chemokine co  
 XX -receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its  
 XX derivative. Other viral infections can also be treated using the method.  
 XX The present sequence is a peptide derived from HIV and useful in the  
 XX method of the invention

XX Sequence 36 AA;

Query Match 100.0%; Score 192; DB 5; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-16;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36  
 |||||  
 Db 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

## RESULT 13

ADE02854  
 ID ADE02854 standard; peptide; 36 AA.

XX ADE02854;

XX DT 29-JAN-2004 (first entry)

XX DE Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID NO 1361.

XX KW hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;  
 XX pharmacokinetic; fusogenic; insulin; diabetes.

```
OS Unidentified.
XX USG348568-B1.
PN
XX 19-FEB-2002.
PD
XX
XX 20-MAY-1999; 99US-00315304.
PF
XX
XX 20-MAY-1998; 98US-00082279.
PR
XX
XX (TRIM-) TRIMERIS INC.
PA
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
PI
XX WPI; 2002-424396/45.
DR
XX
XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral
PT activity, has enhancer peptide sequence derived from retroviral envelope
PT protein sequences linked to core polypeptide e.g. therapeutic protein.
PT
XX
PS Disclosure; SEQ ID NO 1361; 70pp; English.
XX
XX The invention relates to a novel hybrid polypeptide comprising an
CC enhancer peptide sequence linked to a core polypeptide. The enhancer
CC peptide sequence comprises WQWEQKI or WASLWFW. The invention also
CC includes novel peptides that exhibit anti-fusogenic activity, antiviral
CC activity and/or ability to modulate intracellular processes. The novel
CC hybrid polypeptide has virucide and antidiabetic activity. The enhancer
CC peptide sequence enhances pharmacokinetic properties of any core
CC polypeptide, for example, a polypeptide useful for the treatment or
CC prevention of a disease, or an imaging agent useful for imaging
CC structures in vivo. The core polypeptides and hybrid polypeptides are
CC useful for modulating fusogenic events and exhibit antifusogenic or
CC antiviral activity. The novel hybrid polypeptide is useful for decreasing
CC viral infection and modulating intracellular processes involving coiled-
CC coil peptide interactions. The novel hybrid polypeptide comprises insulin
CC or its fragment, so the core polypeptide is useful for ameliorating the
CC symptoms of forms of diabetes. The novel hybrid polypeptide is also
CC useful as a part of prognosis for preventing disorders including fusion
CC events and viral infection that involves cell-cell and/or virus-cell
CC fusion, and for diagnosis and in vivo imaging methods. This sequence
CC represents an enhancer peptide of the invention.
XX
XX Sequence 36 AA;
SQ
Query Match 100.0%; Score 192; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTSLIYSLLKSKIQQEKNEQELLELDKWSLWNWF 36
Db 1 YTSLIYSLLKSKIQQEKNEQELLELDKWSLWNWF 36
RESULT 14
ADE02853
ID ADE02853 standard; peptide; 36 AA.
XX
XX ADE02853;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX
XX Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID NO 1360.
DE
XX
XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;
KW pharmacokinetic; fusogenic; insulin; diabetes.
KW
XX
XX Unidentified.
OS
XX
XX Key Location/Qualifiers
FH
XX
XX Modified-site 1
FT
XX
XX Modified-site 36
FT
/Note= "Residue is modified by acetyl group"
XX
```

```
FT
XX USG348568-B1.
PN
XX 19-FEB-2002.
PD
XX
XX 20-MAY-1999; 99US-00315304.
PF
XX
XX 20-MAY-1998; 98US-00082279.
PR
XX
XX (TRIM-) TRIMERIS INC.
PA
XX
XX Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;
PI
XX WPI; 2002-424396/45.
DR
XX
XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral
PT activity, has enhancer peptide sequence derived from retroviral envelope
PT protein sequences linked to core polypeptide e.g. therapeutic protein.
PT
XX
PS Disclosure; SEQ ID NO 1360; 70pp; English.
XX
XX The invention relates to a novel hybrid polypeptide comprising an
CC enhancer peptide sequence linked to a core polypeptide. The enhancer
CC peptide sequence comprises WQWEQKI or WASLWFW. The invention also
CC includes novel peptides that exhibit anti-fusogenic activity, antiviral
CC activity and/or ability to modulate intracellular processes. The novel
CC hybrid polypeptide has virucide and antidiabetic activity. The enhancer
CC peptide sequence enhances pharmacokinetic properties of any core
CC polypeptide, for example, a polypeptide useful for the treatment or
CC prevention of a disease, or an imaging agent useful for imaging
CC structures in vivo. The core polypeptides and hybrid polypeptides are
CC useful for modulating fusogenic events and exhibit antifusogenic or
CC antiviral activity. The novel hybrid polypeptide is useful for decreasing
CC viral infection and modulating intracellular processes involving coiled-
CC coil peptide interactions. The novel hybrid polypeptide comprises insulin
CC or its fragment, so the core polypeptide is useful for ameliorating the
CC symptoms of forms of diabetes. The novel hybrid polypeptide is also
CC useful as a part of prognosis for preventing disorders including fusion
CC events and viral infection that involves cell-cell and/or virus-cell
CC fusion, and for diagnosis and in vivo imaging methods. This sequence
CC represents an enhancer peptide of the invention.
XX
XX Sequence 36 AA;
SQ
Query Match 100.0%; Score 192; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YTSLIYSLLKSKIQQEKNEQELLELDKWSLWNWF 36
Db 1 YTSLIYSLLKSKIQQEKNEQELLELDKWSLWNWF 36
RESULT 15
ADN06925
ID ADN06925 standard; protein; 36 AA.
XX
XX ADN06925;
AC
XX
XX 17-JUN-2004 (first entry)
DT
XX
XX Peptide #36 used in the pharmaceutical composition of the invention.
DE
XX
XX Pharmaceutical; human immunodeficiency virus; HIV; gp41; glycoprotein41;
KW HIV infection; antiviral; therapy.
KW
XX
XX Unidentified.
OS
XX
XX US2004063637-A1.
PN
XX
XX 01-APR-2004.
PD
XX
```



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OM protein - protein\_search, using sw model

Run on: March 6, 2006, 15:37:45 ; Search time 18.3333 Seconds  
(without alignments)  
188.935 Million cell updates/sec

Title: US-09-809-060A-4  
Perfect score: 192  
Sequence: 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWLWNP 36

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 11837

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80.\*  
1: Pirl.\*  
2: Pirl2.\*  
3: Pirl3.\*  
4: Pirl4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	20.8	36	2 A34594	myosin regulatory
2	39	20.3	30	2 H70152	hypothetical prote
3	38	19.8	31	2 I50390	myosin light chain
4	37	19.3	45	2 T52125	R2R3-MYB transcrip
5	36	18.8	24	2 S01808	hemoglobin AII - t
6	36	18.8	30	2 I77411	renin-2 - mouse (f
7	36	18.8	38	2 C92373	hypothetical prote
8	36	18.8	45	2 S01814	hemoglobin BII - t
9	35	18.2	33	2 A82186	hypothetical prote
10	35	18.2	36	2 D83682	hypothetical prote
11	35	18.2	42	2 T07291	hypothetical prote
12	35	18.2	47	2 C81237	hypothetical prote
13	35	18.2	49	2 T06923	high light-inducib
14	35	18.2	50	2 E90557	hypothetical prote
15	35	18.2	50	2 F86472	5.7K hypothetical
16	34.5	18.0	48	2 S35693	cystic fibrosis tr
17	34	17.7	40	2 S77777	hypothetical prote
18	34	17.7	41	2 T07274	hypothetical prote
19	34	17.7	41	2 T48342	hypothetical prote
20	34	17.7	45	2 S28565	hypothetical prote
21	34	17.7	47	2 G84083	hypothetical prote
22	34	17.7	50	2 P00026	photosystem I 9K p
23	33.5	17.4	43	2 B83894	hypothetical prote
24	33.5	17.4	47	2 S31005	gene 60 protein -
25	33	17.2	33	2 S23321	hypothetical prote
26	33	17.2	43	2 S21282	thymosin beta-11 -
27	33	17.2	43	2 S21694	thymosin beta-12 -
28	33	17.2	48	2 D83774	hypothetical prote
29	33	17.2	50	2 T06541	probable NADPH-fer

30 32.5 16.9 46 2 D90534  
31 32.5 16.9 49 2 A37405  
32 32 16.7 43 1 TNBOB4  
33 32 16.7 43 2 T07503  
34 32 16.7 43 2 H83653  
35 32 16.7 44 1 A38682  
36 32 16.7 44 1 TNRTB4  
37 32 16.7 49 2 E97287  
38 32 16.7 49 2 F70221  
39 32 16.7 50 1 A37217  
40 32 16.7 50 2 A90573  
41 31 16.1 25 2 S68897  
42 31 16.1 28 1 LFSEW  
43 31 16.1 29 2 E33208  
44 31 16.1 31 2 H82533  
45 31 16.1 32 2 S20771

ribosomal protein  
androgen-binding p  
thymosin beta-4 -  
hypothetical prote  
hypothetical prote  
thymosin beta-4 (v  
thymosin beta-4 -  
L33 protein (impor  
hypothetical prote  
thymosin beta-4 -  
50S ribosomal prot  
phospholipase A2 (  
trp operon leader  
calreticulin, uter  
hypothetical prote  
Ig heavy chain V r

## ALIGNMENTS

## RESULT 1

A34594  
myosin regulatory light chain - bovine (fragment)  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 29-Jun-1990 #sequence\_revision 05-Apr-1995 #text\_change 09-Jul-2004  
C:Accession: A34594; A31967  
R:Ikebe, M.; Reardon, S.  
Biochemistry 29, 2713-2720, 1990  
A:Title: Phosphorylation of bovine platelet myosin by protein kinase C.  
A:Reference number: A34594; MUID:90268021; PMID:2346743  
A:Accession: A34594  
A:Molecule type: protein  
A:Residues: 1-33, 'X', 35-36 <IKE>  
A:Cross-references: UNIPROT:Q7M2V5; UNIPARC:UPI00001776D9  
A:Experimental source: Platelet  
R:Colburn, J.C.; Michnoff, C.H.; Hsu, L.C.; Slaughter, C.A.; Kamm, K.E.; Stull, J.T.  
J. Biol. Chem. 263, 19166-19173, 1988  
A:Title: Sites phosphorylated in myosin light chain in contracting smooth muscle.  
A:Reference number: A31967; MUID:89066722; PMID:3198618  
A:Accession: A31967  
A:Molecule type: protein  
A:Residues: 17-34 <COL>  
A:Cross-references: UNIPARC:UPI00001776DA  
A:Experimental source: smooth muscle  
C:Superfamily: calmodulin; calmodulin repeat homology  
C:Keywords: blocked amino end; EF hand; phosphoprotein  
F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental  
F:1/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experimental  
F:2/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status experimental  
F:9/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status experimental  
F:18/Binding site: phosphate (Thr) (covalent) (by myosin-light-chain kinase) (partial) #  
F:19/Binding site: phosphate (Ser) (covalent) (by myosin-light-chain kinase) #status exp

Query Match 20.8%; Score 40; DB 2; Length 36;  
Best Local Similarity 41.2%; Pred. No. 1.8e+02;  
Matches 7; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Oy 2 TSLIYSLLEKSIQIQEK 18  
|||:::|||||:  
Db 18 TSNVFAMFDQSIQEFK 34

## RESULT 2

H70152  
hypothetical protein B80425 - Lyme disease spirochete  
C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
C:Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C:Accession: H70152  
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horat, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997

A;Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-45 <RO2>  
A:Cross-references: UNIPARC:UPI000016DC6F; EMBL:Z95788; PIDN:CAB09220.1  
C:Genetics:  
A:Gene: MYB56; MYB65

Query Match 19.3%; Score 37; DB 2; Length 45;  
Best Local Similarity 34.5%; Pred.No. 5.5e+02;  
Matches 10; Conservative 7; Mismatches 6; Indels 2;

Qy 9 LEKSQIQEQKNEQEELLE-----DKWASL 32  
|: ||||| :||| :||| :  
Db 11 LKKGAFSQBE-EQLIVEMHAKGNKWAQM 38  
|: ||||| :||| :||| :

RESULT 5  
S01808  
hemoglobin AII - tube worm (Lamellibrachia sp.) (fragment)  
C:Species: Lamellibrachia sp.  
C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
C:Accession: S01808  
R:Suzuki, T.; Takagi, T.; Ohta, S.  
Biochem. J. 255, 541-545, 1988  
A:Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably  
A:Reference number: S01807; MUID:89076216; PMID:3202832  
A:Accession: S01808  
A:Molecule type: protein  
A:Residues: 1-24 <SUZ>  
A:Cross-references: UNIPROT:Q9TWS6; UNIPARC:UPI000017711B  
C:Keywords: oxygen carrier

Query Match 18.8%; Score 36; DB 2; Length 24;  
Best Local Similarity 26.3%; Pred.No. 3.6e+02;  
Matches 5; Conservative 8; Mismatches 2; Indels 4; Gaps 1;

Qy 16 QEKNEQEELDELDKWASLWN 34  
::: |::| :||::|  
Db 8 EDRREMQLM----WANVWS 22  
|: ||||| :||| :||| :

RESULT 6  
I77411  
renin-2 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Oct-2004  
C:Accession: I77411  
R:Field, L.J.; Philbrick, W.M.; Howles, P.N.; Dickinson, D.P.; McGowan, R.A.; Grosse, K.W.  
Mol. Cell. Biol. 4, 2321-2331, 1984  
A:Title: Expression of tissue-specific Ren-1 and Ren-2 genes of mice: Comparative analysis  
A:Reference number: I57576; MUID:85085936; PMID:6392850  
A:Accession: I77411  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-30 <RES>  
A:Cross-references: UNIPROT:P00796; UNIPARC:UPI000016C94B; GB:K02801; NID:g200695; PIDN:  
C:Superfamily: Pepsin

Query Match 18.8%; Score 36; DB 2; Length 30;  
Best Local Similarity 71.4%; Pred.No. 4.6e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 29 WASLNNW 35  
||| ||| |  
Db 9 WALLWLW 15  
|: ||||| :||| :||| :

RESULT 7  
C82373  
hypothetical protein VC0017 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C:Species: Vibrio cholerae  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: C82373

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R.  
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: C82373  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-38 <HEI>  
A:Cross-references: UNIPROT:Q9KX1; UNIPARC:UPI00000C2B91; GB:AE004094; GB:AE003852; NID  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC0017  
A:Map position: 1

Query Match 18.8% Score 36; DB 2; Length 38;  
Best Local Similarity 46.7%; Pred. No. 6e+02;  
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 7 SLLEKSIQIQEKNEQ 21  
||| :||| :  
DB 12 SLKEKRLKQEKAGE 26

RESULT 8  
S01814  
hemoglobin BII - tube worm (*Lamellibrachia* sp.) (fragment)  
C:Species: *Lamellibrachia* sp.  
C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-May-2004  
C:Accession: S01814  
R;Suzuki, T.; Takagi, T.; Ohta, S.  
Biochem. J. 255, 541-545, 1988  
A:Title: N-terminal amino acid sequence of the deep-sea tube worm haemoglobin remarkably  
A:Reference number: S01807; MUID:89076216; PMID:3202832  
A:Accession: S01814  
A:Molecule type: protein  
A:Residues: 1-45 <SUZ>  
A:Cross-references: UNIPARC:UPI000017711A  
C:Keywords: oxygen carrier

Query Match 18.8% Score 36; DB 2; Length 45;  
Best Local Similarity 26.3%; Pred. No. 7.2e+02;  
Matches 5; Conservative 8; Mismatches 2; Indels 4; Gaps 1;

QY 16 QEKNEQELLEDKWASLWN 34  
::: |:|: ||::|:  
DB 8 EDRREMQLM----WANVWS 22

RESULT 9  
A82186  
hypothetical protein VC1559 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)  
C:Species: *Vibrio cholerae*  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C:Accession: A82186  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R.  
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: A82186  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-33 <HEI>  
A:Cross-references: UNIPROT:Q9KRS7; UNIPARC:UPI00000C3017; GB:AE004233; GB:AE003852; NID  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC1559  
A:Map position: 1

Query Match 18.2% Score 35; DB 2; Length 33;

Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V  
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain Mc58.  
A:Reference number: A81000; MUID:20175755; PMID:10710307

A:Accession: C01237  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-47 <TET>  
A:Cross-references: UNIPROT:Q9K1L4; UNIPARC:UPI000000C43EE; GB:AE002098; NID  
A:Experimental source: serogroup B, strain Mc58  
C:Genetics:  
A:Gene: NMB0099

Query Match 18.2%; Score 35; DB 2; Length 47;  
Best Local Similarity 37.5%; Pred. No. 1.le+03;  
Matches 9; Conservative 3; Mismatches 8; Indels 4; Gaps 1;

Qy 10 EKSQIQ---EKNEQEELLELDKW 29  
:|||||:|:|:|  
Db 20 KKQIQQKKETKSPKHKASRDW 43

RESULT 13  
T06923  
high light-inducible protein homolog - Cyanophora paradoxa cyanelle  
C:Species: cyanelle Cyanophora paradoxa  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T06923  
R:Stirewalt, V.L.; Michalowski, C.B.; Luffelhardt, W.; Bohnert, H.J.; Bryant, D.A.  
submitted to the EMBL Data Library, July 1995  
A:Description: Nucleotide sequence of the cyanelle genome from *Cyanophora paradoxa*.  
A:Reference number: Z15840  
A:Accession: T06923

A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-49 <STI>  
A:Cross-references: UNIPROT:P48367; UNIPARC:UPI000013A441; EMBL:U30821; NID:G1016083; PI  
A:Experimental source: strain Pringsheim LB555  
C:Genetics:  
A:Gene: ycf17  
A:Genome: cyanelle  
C:Superfamily: high light-inducible protein ssl2542  
C:Keywords: cyanelle

Query Match 18.2%; Score 35; DB 2; Length 49;  
Best Local Similarity 27.3%; Pred. No. 1.le+03;  
Matches 6; Conservative 4; Mismatches 0; Indels 12; Gaps 1;

Qy 14 IQEKNQEELLELDKWASLWNW 35  
:|||||:|:|:|  
Db 1 MQEERN-----IWNW 10

RESULT 14  
E90557  
hypothetical protein MYPV 3650 [imported] - Mycoplasma pulmonis (strain UAB CTIP)  
C:Species: Mycoplasma pulmonis  
C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
C:Accession: E90557  
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;  
Nucleic Acids Res. 29, 2145-2153, 2001  
A:Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulm*  
A:Reference number: A99512; MUID:21267165; PMID:11353084  
A:Accession: E90557  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-50 <KUR>  
A:Cross-references: UNIPROT:Q98QJ6; UNIPARC:UPI000000C8071; GB:AL445566; PID:G14089779; F  
A:Experimental source: strain UAB CTIP  
C:Genetics:  
A:Gene: MYPV\_3650  
A:Genetic code: SGC3

Query Match 18.2%; Score 35; DB 2; Length 50;  
Best Local Similarity 33.3%; Pred. No. 1.le+03;  
Matches 8; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 5 IYSLLEKSIQOEKNEQEELLELDK 28  
:|||||:|:|:|  
Db 6 LYENIKKEIKYKNSIVLNEFKK 29

RESULT 15  
F86472  
5.7K hypothetical protein T3269.50 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: F86472

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansan, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J.  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F86472  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-50 <STO>  
A:Cross-references: UNIPROT:Q9C6E9; UNIPARC:UPI000000A80F1; GB:AE005172; NID:G11386311; P:  
C:Genetics:  
A:Map position: 1

Query Match 18.2%; Score 35; DB 2; Length 50;  
Best Local Similarity 38.1%; Pred. No. 1.le+03;  
Matches 8; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

Qy 7 SLLEKSIQOEKNEQEELLELD 27  
:|||||:|:|:|  
Db 17 SYQESSESESEDEETESD 37

Search completed: March 6, 2006, 15:44:17  
Job time : 19:3333 secs





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NCBI_TaxID=11676;
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RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06726; AAA19139.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 49
FT NON TER 49 49
SQ SEQUENCE 49 AA; 6167 MW; 0277C4815B8D26FE CRC64;

Query Match 94.3%; Score 181; DB 2; Length 49;
Best Local Similarity 91.7%; Pred. No. 1.1e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSOIQEKNQELLEDKQASLWNWF 36
Db 14 YTGLIYTLLEESQIQEKNQELLEDKQASLWNWF 49

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Q69909_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69909;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
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RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06739; AAA19152.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 49
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SQ SEQUENCE 49 AA; 6196 MW; E9B618025B932D1E CRC64;

Query Match 92.7%; Score 178; DB 2; Length 49;
Best Local Similarity 91.7%; Pred. No. 2.5e-14;
Matches 33; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSOIQEKNQELLEDKQASLWNWF 36
Db 14 YTGLIYTLLEESQIQEKNQELLEDKQASLWNWF 49

RESULT 4
Q69906_9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69906;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06740; AAA19153.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 42
FT NON TER 42 42
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Query Match 91.7%; Score 176; DB 2; Length 42;
Best Local Similarity 88.9%; Pred. No. 3.7e-14;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSOIQEKNQELLEDKQASLWNWF 36
Db 7 YTSLIYTLLEESQIQEKNQELLEDKQASLWNWF 42

RESULT 5
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AC Q69906;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
[1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06736; AAA19149.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 49
FT NON TER 49 49
SQ SEQUENCE 49 AA; 6214 MW; 29C4E5A8CBD63DD8 CRC64;
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Q69910_9HIV1 PRELIMINARY; PRT; 42 AA.
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06740; AAA19153.1; -; mRNA.
DR HSSP; P31872; 1LB0.
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 42
FT NON TER 42 42
SQ SEQUENCE 42 AA; 5248 MW; 613E1B2DBB31A722 CRC64;

Query Match 91.7%; Score 176; DB 2; Length 42;
Best Local Similarity 88.9%; Pred. No. 3.7e-14;
Matches 32; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSOIQEKNQELLEDKQASLWNWF 36
Db 7 YTSLIYTLLEESQIQEKNQELLEDKQASLWNWF 42

RESULT 5
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AC Q69906;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
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RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR EMBL; U06736; AAA19149.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON TER 1 49
FT NON TER 49 49
SQ SEQUENCE 49 AA; 6214 MW; 29C4E5A8CBD63DD8 CRC64;
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OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
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RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06724; AAA19137.1; -; mRNA.
DR HSSP; P31872; 1LB0.
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DR GO; GO:0019031; C:viral envelope; IEA.
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Best Local Similarity 90.9%; Pred. No. 2.9e-13;
Matches 30; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Db 2 LIYTLLESQVQOEKNEQELLELDKWASLWNWF 34
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AC Q69905;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
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RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
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SQ SEQUENCE 34 AA; 4196 MW; 7B72A8EA164B99C CRC64;

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Best Local Similarity 93.9%; Pred. No. 5e-13;
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Db 2 LIYTLLESQVQOEKNEQELLELDKWASLWNWF 34
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06728; AAA19141.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
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DR Pfam; PF00517; GP41; 1.
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FT NON_TER 50 50
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06733; AAA19146.1; -; mRNA.
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DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1 34
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 4226 MW; E609273F6164BD80 CRC64;

Query Match 85.4%; Score 164; DB 2; Length 34;
Best Local Similarity 88.2%; Pred. No. 8.9e-13;
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SLIYSLLKSKIQOEKNEQELLELDKWASLWNWF 36
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RESULT 12
Q69898_9HIV1 PRELIMINARY; PRT; 50 AA.
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
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RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT monoclonal antibody.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06728; AAA19141.1; -; mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
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DR Pfam; PF00517; GP41; 1.
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:43:35 ; Search time 27.6667 Seconds  
(without alignments)  
107.578 Million cell updates/sec

Title: US-09-809-060A-4  
Perfect score: 192  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 308952

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Maximum DB seq length: 50
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	192	100.0	36	2	US-08-484-223B-240	Sequence 240, App
2	192	100.0	36	2	US-09-082-279B-1360	Sequence 1360, Ap
3	192	100.0	36	2	US-09-315-304B-1360	Sequence 1360, Ap
4	192	100.0	36	2	US-09-834-784-1360	Sequence 1360, Ap
5	192	100.0	36	2	US-09-515-965A-1360	Sequence 1360, Ap
6	192	100.0	36	2	US-09-350-641C-1360	Sequence 1360, Ap
7	192	100.0	36	2	US-09-350-841A-1360	Sequence 1360, Ap
8	189	98.4	36	2	US-09-082-279B-1361	Sequence 1361, Ap
9	189	98.4	36	2	US-09-315-304B-1361	Sequence 1361, Ap
10	189	98.4	36	2	US-09-834-784-1361	Sequence 1361, Ap
11	189	98.4	36	2	US-09-515-965A-1361	Sequence 1361, Ap
12	189	98.4	36	2	US-09-350-641C-1361	Sequence 1361, Ap
13	189	98.4	36	2	US-09-350-841A-1361	Sequence 1361, Ap
14	187	97.4	36	1	US-08-073-028-5	Sequence 5, Appli
15	187	97.4	36	2	US-08-486-099-5	Sequence 5, Appli
16	187	97.4	36	2	US-08-360-107A-5	Sequence 5, Appli
17	187	97.4	36	2	US-08-484-223B-5	Sequence 5, Appli
18	187	97.4	36	2	US-08-919-591-5	Sequence 5, Appli
19	187	97.4	36	2	US-08-475-668A-5	Sequence 5, Appli
20	187	97.4	36	2	US-08-485-551A-5	Sequence 5, Appli
21	187	97.4	36	2	US-08-471-913A-5	Sequence 5, Appli
22	187	97.4	36	2	US-08-554-616-5	Sequence 5, Appli
23	187	97.4	36	2	US-08-485-264A-5	Sequence 5, Appli
24	187	97.4	36	2	US-08-474-349A-5	Sequence 5, Appli
25	187	97.4	36	2	US-08-255-208A-5	Sequence 5, Appli
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27	187	97.4	36	2	US-08-470-896-5	Sequence 5, Appli

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## ALIGNMENTS

## RESULT 1

US-08-484-223B-240  
 ; Sequence 240, Application US/08484223B  
 ; Patent No. 6020459  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bolognesi, Dani P.  
 ; APPLICANT: Matthews, Thomas J.  
 ; APPLICANT: Wild, Carl T.  
 ; APPLICANT: Barney, Shawn O.  
 ; APPLICANT: Lambert, Dennis M.  
 ; APPLICANT: Patteway, Stephen R.  
 ; APPLICANT: Langlois, Alphonse J.  
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
 ; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
 ; TITLE OF INVENTION: TRANSMISSION  
 ; NUMBER OF SEQUENCES: 245  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds LLP  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/484, 223B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-029  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 240:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
1-484-223B-240

Query Match 100.0%; Score 192; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 1e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSIIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36  
Db 1 YTSIIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

## RESULT 2

US-09-082-279B-1360  
; Sequence 1360, Application US/09082279B

; Patent No. 6258782

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/082,279B

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-082-279B-1360

Query Match 100.0%; Score 192; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSIIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36  
Db 1 YTSIIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

## RESULT 3

US-09-315-304B-1360

; Sequence 1360, Application US/09315304B

; Patent No. 6348568

; GENERAL INFORMATION:

; APPLICANT: Barney, S.

; APPLICANT: Guthrie, K.

; APPLICANT: Merutka, G.

; APPLICANT: Anwer, M.

; APPLICANT: Lambert, D.

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

; FILE REFERENCE: 7872-052

; CURRENT APPLICATION NUMBER: US/09/315,304B

; PRIOR FILING DATE: 1999-05-20

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1667

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-315-304B-1360

Query Match 100.0%; Score 192; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSIIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36  
Db 1 YTSIIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

## RESULT 4

US-09-834-784-1360

; Sequence 1360, Application US/09834784

; Patent No. 8562787

; GENERAL INFORMATION:

; APPLICANT: Barney, Shawn

; APPLICANT: Guthrie, Kelly

; APPLICANT: Merutka, Gene

; APPLICANT: Anwer, Mohamed

; APPLICANT: Lambert, Dennis

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED

; FILE REFERENCE: 7872-043

; CURRENT APPLICATION NUMBER: US/09/834,784

; PRIOR FILING DATE: 2001-04-13

; PRIOR APPLICATION NUMBER: 09/082,279

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1515

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-834-784-1360

Query Match 100.0%; Score 192; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSIIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36  
Db 1 YTSIIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

## RESULT 5

US-09-515-965A-1360

; Sequence 1360, Application US/09515965A

; Patent No. 8623741

; GENERAL INFORMATION:

; APPLICANT: Antczak, J.

; APPLICANT: Delmedico, M.

; APPLICANT: Erickson, J.

; APPLICANT: Lambert, D.

; APPLICANT: Siata, P.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-

; FILE REFERENCE: 7872-073

; CURRENT APPLICATION NUMBER: US/09/515,965A

; PRIOR FILING DATE: 2000-02-29

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/082,279

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1994

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-515-965A-1360

Query Match 100.0%; Score 192; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 1e-16;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



**Qy**      1 YTSLSLEKSIQQEKNEQELLELDKWASLWNWF 36  
**Dd**      1 YTSLSLEKSIQQEKNEQELLELDKWASLWNWF 36	

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RESULT 6
US-09-350-641C-1360
/ Sequence 1360, Application US/09350641C
/ Patent No. 6656906
/ GENERAL INFORMATION:
/ APPLICANT: Barney, S.
/ APPLICANT: Guthrie, K.
/ APPLICANT: Merutka, G.
/ APPLICANT: Anwer, M.
/ APPLICANT: Lambert, D.
/ TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
/ TITLE OF INVENTION: PROPERTIES
/ FILE REFERENCE: 7872-067
/ CURRENT APPLICATION NUMBER: US/09/350,641C
/ CURRENT FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: 09/315,304
/ PRIOR FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: 09/082,279
/ PRIOR FILING DATE: 1998-05-20
/ NUMBER OF SEQ ID NOS: 1757
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1360
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Core polypeptide
US-09-350-641C-1360

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Query Match      100.0%; Score 192; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 YTSLSLLEKSIQOQKNEQELLELDKQASLWNWF 36  
|||

Db 1 YTSLSLLEKSIQOQKNEQELLELDKQASLWNWF 36  
|||

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RESULT 7
US-09-350-841A-1360
; Sequence 1360, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffs, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1360
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-841A-1360

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Query Match      100.0%; Score 192; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e-16;
Matches 36: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 YTSIIYSLLKSKIQQEKNEQELLELDKQASLWNWF 36  
|||||

Db 1 YTSIIYSLLKSKIQQEKNEQELLELDKQASLWNWF 36  
|||||

RESULT 8  
US-09-082-2798-1361  
; Sequence 1361, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merrucka, Gene  
; APPLICANT: Anwer, Mohammed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082,279B  
; CURRENT FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1361  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-082-2798-1361

Query Match 98.4%; Score 189; DB 2; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.4e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**Qy**

1 YTSIYSLLEKSIQQEKNEQELLELDKWASLWNWF 36  
|||||

**Db**

1 YTSIYSLLEKSIQQEKNEQELLELDKWASLWNWF 36  
|||||

```

RESULT 9
US-09-315-304B-1361
/ Sequence 1361, Application US/09315304B
/ Patent No. 6348568
/ GENERAL INFORMATION:
/ APPLICANT: Barney, S.
/ APPLICANT: Guthrie, K.
/ APPLICANT: Merutka, G.
/ APPLICANT: Anwer, M.
/ APPLICANT: Lambert, D.
/ TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
/ TITLE OF INVENTION: PROPERTIES
/ FILE REFERENCE: 7872-052
/ CURRENT APPLICATION NUMBER: US/09/315,304B
/ CURRENT FILING DATE: 1999-05-20
/ PRIOR APPLICATION NUMBER: 09/082,279
/ PRIOR FILING DATE: 1998-05-20
/ NUMBER OF SEQ ID NOS: 1667
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 1361
/ LENGTH: 36
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Core polypeptide
US-09-315-304B-1361

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Query Match 98.4%; Score 189; DB 2; Length 36;  
Best Local Similarity 97.2%; Pred. No. 2.4e-16;  
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

**Qy**,  
1 YTSIIYSLLEKSIQQEKNEQELLELDKWASLWNWF 36  
|||||

**Dd**  
1 YTSIIYSLLEKSIQQEKNEQELLELDKWASLWNWF 36  
|||||

RESULT 10  
US-09-834-784-1361



APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV  
TITLE OF INVENTION: TRANSMISSION  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,028  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-004-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: Peptide  
US-08-073-028-5

Query Match 97.4%; Score 187; DB 1; Length 36;  
Best Local Similarity 97.2%; Pred. No. 4.2e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36  
|||||  
Db 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36

## RESULT 15

US-08-486-099-5  
Sequence 5, Application US/08486099  
Patent No. 6013263  
GENERAL INFORMATION:  
APPLICANT: Bolognesi, Dani P.  
APPLICANT: Matthews, Thomas J.  
APPLICANT: Wild, Carl T.  
APPLICANT: Barney, Shawn O.  
APPLICANT: Lambert, Dennis M.  
APPLICANT: Petteway, Stephen R.  
APPLICANT: Langlois, Alphonse J.  
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS  
TITLE OF INVENTION: B VIRUS TRANSMISSION  
NUMBER OF SEQUENCES: 209  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,099  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7872-031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 36 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-486-099-5

Query Match 97.4%; Score 187; DB 2; Length 36;  
Best Local Similarity 97.2%; Pred. No. 4.2e-16;  
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36  
|||||  
Db 1 YTSLIYSLLEKSOIQQEKNEQELLELDKWASLWNWF 36

Search completed: March 6, 2006, 15:45:44  
Job time : 27.6667 secs

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OM protein - protein search, using sw model

Run on: March 6, 2006, 15:44:30 ; Search time 94 Seconds  
(without alignments)  
160.020 Million cell updates/sec

Title: US-09-809-060A-4  
Perfect score: 192  
Sequence: 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36

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Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
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6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	192	100.0	36	3	US-09-809-060-4
2	192	100.0	36	4	US-10-351-641-1360
3	192	100.0	36	4	US-10-663-589-40
4	192	100.0	36	4	US-10-671-282-40
5	192	100.0	36	5	US-10-168-295-5
6	192	100.0	36	5	US-10-168-295-57
7	189	98.4	36	4	US-10-351-641-1361
8	187	97.4	36	4	US-10-252-136-5
9	187	97.4	36	4	US-10-267-682-5
10	187	97.4	36	4	US-10-267-748-5
11	187	97.4	36	4	US-10-950-010-5
12	187	97.4	36	6	US-11-066-697-1423
13	181	94.3	36	4	US-10-351-641-1749
14	179	93.2	36	4	US-10-351-641-642
15	179	93.2	36	4	US-10-457-780-52
16	179	93.2	36	5	US-10-950-010-537
17	178	92.7	36	4	US-10-351-641-643
18	178	92.7	46	3	US-09-854-816-112
19	176	91.7	36	5	US-10-950-010-541
20	176	91.7	38	4	US-10-351-641-1509
21	175	91.1	36	4	US-10-351-641-1249
22	175	91.1	36	4	US-10-351-641-1424
23	175	91.1	36	4	US-10-351-641-1751
24	174	90.6	36	3	US-09-809-060-1
25	174	90.6	36	3	US-09-809-060-85
26	174	90.6	36	3	US-09-796-202-10
27	174	90.6	36	3	US-09-960-717-2

28 174 90.6 36 3 US-09-779-451-5 Sequence 5, Appli  
29 174 90.6 36 3 US-09-834-628-1 Sequence 1, Appli  
30 174 90.6 36 3 US-09-828-615-1 Sequence 1, Appli  
31 174 90.6 36 3 US-09-854-816-1 Sequence 1, Appli  
32 174 90.6 36 3 US-09-854-816-108 Sequence 108, App  
33 174 90.6 36 3 US-09-874-475-16 Sequence 16, Appli  
34 174 90.6 36 3 US-09-493-246-1 Sequence 1, Appli  
35 174 90.6 36 4 US-10-116-797-1 Sequence 1, Appli  
36 174 90.6 36 4 US-10-252-136-37 Sequence 37, Appli  
37 174 90.6 36 4 US-10-252-136-39 Sequence 39, Appli  
38 174 90.6 36 4 US-10-158-742A-8 Sequence 8, Appli  
39 174 90.6 36 4 US-10-323-314-10 Sequence 10, Appli  
40 174 90.6 36 4 US-10-278-364A-7 Sequence 7, Appli  
41 174 90.6 36 4 US-10-351-641-15 Sequence 15, Appli  
42 174 90.6 36 4 US-10-351-641-211 Sequence 211, App  
43 174 90.6 36 4 US-10-351-641-497 Sequence 497, App  
44 174 90.6 36 4 US-10-351-641-498 Sequence 498, App  
45 174 90.6 36 4 US-10-351-641-498 Sequence 498, App

## ALIGNMENTS

RESULT 1  
US-09-809-060-4  
; Sequence 4, Application US/09809060  
; Publication No. US2002010317A1  
; GENERAL INFORMATION:  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Allaway, Graham P.  
; TITLE OF INVENTION: A Method for Generating Immunogens that Elicit  
; TITLE OF INVENTION: Neutralizing Antibodies against Fusion-Active  
; TITLE OF INVENTION: Regions of HIV Envelope Proteins  
; FILE REFERENCES: 1900.0260001  
; CURRENT APPLICATION NUMBER: US/09/809,060  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: US 60/189,981  
; PRIOR FILING DATE: 2000-03-17  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 4  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-09-809-060-4

Query Match 100.0%; Score 192; DB 3; Length 36;  
Best Local Similarity 100.0%; Pred. No. 36-15;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36  
DB 1 YTSLIYSLLEKSIQOEKNEQELLELDKWASLWNWF 36

RESULT 2  
US-10-351-641-1360  
; Sequence 1360, Application US/10351641  
; Publication No. US20030186874A1  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCES: 7872-100  
; CURRENT APPLICATION NUMBER: US/10/351,641  
; CURRENT FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 09/350,641  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/315,304

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; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1360
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1360

Query Match      100.0%; Score 192; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 3
US-10-663-589-40
; Sequence 40, Application US/10663589
; Publication No. US2004006367A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-40

Query Match      100.0%; Score 192; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 4
US-10-671-282-40
; Sequence 40, Application US/10671282
; Publication No. US20040122214A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
; FILE REFERENCE: TRM-004
; CURRENT APPLICATION NUMBER: US/10/671,282
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/414,439
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
```

```
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-671-282-40

Query Match      100.0%; Score 192; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 5
US-10-168-295-5
; Sequence 5, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Batoudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-5

Query Match      100.0%; Score 192; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 6
US-10-168-295-57
; Sequence 57, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Batoudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-57

Query Match      100.0%; Score 192; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36

RESULT 7
US-10-168-295-57
; Sequence 57, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Batoudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-57

Query Match      100.0%; Score 192; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-15;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
   |||||||
Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
```

```
RESULT 7
US-10-351-641-1361
; Sequence 1361, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; FILE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1361
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1361

Query Match          98.4%; Score 189; DB 4; Length 36;
Best Local Similarity 97.2%; Pred. No. 6.8e-15;
Matches 35; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 8
US-10-252-136-5
; Sequence 5, Application US/10252136
; Publication No. US20030103998A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, M. Ross
; APPLICANT: Lambert, Dennis M.
; TITLE OF INVENTION: TREATMENT OF HUMAN IMMUNODEFICIENCY VIRUS AND OTHER
; TITLE OF INVENTION: VIRAL INFECTIONS
; TITLE OF INVENTION: USING COMBINATORY THERAPY
; FILE REFERENCE: 7872-036
; CURRENT APPLICATION NUMBER: US/10/252,136
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/08/973,952
; PRIOR FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-252-136-5

Query Match          97.4%; Score 187; DB 4; Length 36;
Best Local Similarity 97.2%; Pred. No. 1.2e-14;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 9
US-10-267-682-5
; Sequence 5, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennle & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-267-682-5

Query Match          97.4%; Score 187; DB 4; Length 36;
Best Local Similarity 97.2%; Pred. No. 1.2e-14;
Matches 35; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLLKKSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 10
US-10-267-748-5
; Sequence 5, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
```





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; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1749
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1749

Query Match          94.3%; Score 181; DB 4; Length 36;
Best Local Similarity 91.7%; Pred. No. 5,8e-14;
Matches 33; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIHSLIERSQIQQEKNEQELLELDKWASLWNWF 36

RESULT 14
US-10-351-641-642
; Sequence 642, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; CURRENT FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 642
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-642

Query Match          93.2%; Score 179; DB 4; Length 36;
Best Local Similarity 91.7%; Pred. No. 9,9e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLIERSQIQQEKNEQELLELDKWASLWNWF 36
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RESULT 15
US-10-457-780-52
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; Sequence 52, Application US/10457780
; Publication No. US20040137426A1
; GENERAL INFORMATION:
; APPLICANT: SERRES, Pierre-Francois
; APPLICANT: MOSCA, Joseph
; TITLE OF INVENTION: GP41 PEPTIDES AND METHODS BASED THEREON FOR INHIBITING HIV FUSION
; TITLE OF INVENTION: TO TARGET CELLS
; FILE REFERENCE: 118761
; CURRENT APPLICATION NUMBER: US/10/457,780
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/446,268
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/413,919
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/386,754
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Y36F
US-10-457-780-52

Query Match          93.2%; Score 179; DB 4; Length 36;
Best Local Similarity 91.7%; Pred. No. 9,9e-14;
Matches 33; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36
Db 1 YTSLIYSLIERSQIQQEKNEQELLELDKWASLWNWF 36

Search completed: March 6, 2006, 15:50:32
Job time : 95 secs
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; PRIOR APPLICATION NUMBER: 60/539,207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487,964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/459,600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 36
; TYPE: prt
; ORGANISM: Human immunodeficiency vi
US-11-029-003-1

```

Query Match	90.6%	Score 174;	DB 7;	Length 36;
Best Local Similarity	88.9%	Pred. No. 4.2e-16;		
Matches 32; Conservative	3;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	:	1 YTSLIYSLLEKSQIQEKNQEELLEIDKWSLWNWF	36
Db	:	1 YTSLIHSLFEESNQOEKNQEELLEIDKWSLWNWF	36

```

RESULT 3
US-11-187-687-22
; Sequence 22, Application US/11187687
; Publication No. US20060019347A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Ho Sung
; APPLICANT: Daniel, Thomas O.
; APPLICANT: Hays, Anna-Maria
; APPLICANT: Wilson, Troy E.
; APPLICANT: Litzinger, David C.
; APPLICANT: Mariani, Roberto
; APPLICANT: Kimmel, Bruce E.
; APPLICANT: Keefe, William M.
; TITLE OF INVENTION: Biosynthetic Po
; TITLE OF INVENTION: Acids
; FILE REFERENCE: AMBX-0041.00US
; CURRENT APPLICATION NUMBER: US/11/1
; CURRENT FILING DATE: 2008-07-21
; PRIOR APPLICATION NUMBER: 60/590,03
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: 60/659,70
; PRIOR FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency v
US-11-187-687-22

```

Query Match	30.6%	Score 174;	DB 7;	Length 36;
Best Local Similarity	88.9%	Pred. No. 4.2e-16;		
Matches 32; Conservative	3;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	YTSIIYSLLIEKSQIQOEKNEQELLELDKWSLWNWF	36
		: : : : : : : : : : : : : : : : : :	
D6	1	YTSIIHSLIEESNQOEKNEQELLELDKWSLWNWF	36

```

RESULT 4
US-11-112-277-33
; Sequence 33, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Ouraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; TITLE OF INVENTION: CONJUGATES
; FILE REFERENCE: 500862003700

```

```

; CURRENT APPLICATION NUMBER: US/11/112,277
;
; CURRENT FILING DATE: 2005-04-22
;
; PRIOR APPLICATION NUMBER: US 60/565,228
;
; PRIOR FILING DATE: 2004-04-23
;
; NUMBER OF SEQ ID NOS: 53
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 33
;
; LENGTH: 37
;
; TYPE: PRNT
;
; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: T20 Analogue
;
; FEATURE:
;
; NAME/KEY: MOD_RES
;
; LOCATION: 37
;
; OTHER INFORMATION: Xaa is Lys linked to 1
;
; US-11-112-277-33

```

Query Match 90.6%; Score 174; DB 7; Length 37;  
Best Local Similarity 88.9%; Pred. No. 4.3e-16;  
Matches 32; Conservative 3; Mismatches 1; Indels

**Qy**            1 YTSLIYSLLEKSIQIQEKNQEELLELDKWASLWNWF 36  
               |||||:|||:  
**Dd**            1 YTSLIHLSFEESNQOEKNEQELLELDKWASLWNWF 36

```

RESULT 5
US-11-187-687-24
; Sequence 24, Application US/11187687
; Publication No. US20060019347A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Ho Sung
; APPLICANT: Daniel, Thomas G.
; APPLICANT: Hays, Anna-Maria
; APPLICANT: Wilson, Troy E.
; APPLICANT: Litzinger, David C.
; APPLICANT: Mariani, Roberto
; APPLICANT: Kimmel, Bruce E.
; APPLICANT: Keefe, William M.
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino
; FILE OF INVENTION: Acids
; FILE REFERENCE: AMEX-0041.00US
; CURRENT APPLICATION NUMBER: US/11/187,687
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: 60/590,035
; PRIOR FILING DATE: 2004-07-21
; PRIOR APPLICATION NUMBER: 60/659,709
; PRIOR FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 24
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-187-687-24

```

Query Match 90.6%; Score 174; DB 7; Length 44;  
Best Local Similarity 88.9%; Pred. No. 5.2e-16;  
Matches 32; Conservative 3; Mismatches 1; Indels

Qy	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36			
Qy	Y	T	S	L	I	S	L	A	E	K	S	I	Q	E	K	N	E	O	E	L	L	E	J	D	K	W	A	S	I	L	N	W	F						
	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	:	
Db	Y	T	S	L	I	S	L	A	E	K	S	I	Q	E	K	N	E	O	E	L	L	E	J	D	K	W	A	S	I	L	N	W	F						

RESULT 6  
US-11-089-426-10  
; Sequence 10, Application US/11089426  
; Publication No. US20050261229A1  
; GENERAL INFORMATION:  
; APPLICANT: Gillies, Stephen D.  
; APPLICANT: Lo, Kin-Ming

FILE REFERENCE: 500862003700

FILE REFERENCE: 500862003700

```
; APPLICANT: Wesolowski, John
; TITLE OF INVENTION: Fc Fusion Proteins For Enhancing the Immunogenicity of
; TITLE OF INVENTION: Protein and Peptide Antigens
; FILE REFERENCE: LEX-007
; CURRENT APPLICATION NUMBER: US/11/089,426
; CURRENT FILING DATE: 2005-03-24
; PRIOR APPLICATION NUMBER: US/09/621,268
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/144,965
; PRIOR FILING DATE: 1999-07-21
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Fused
; OTHER INFORMATION: polypeptide from pdC-muFC vector
US-11-089-426-10

Query Match      84.4%; Score 162; DB 7; Length 44;
Best Local Similarity 88.2%; Pred. No. 1.8e-14;
Matches 30; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SLIYSLEKSIQIQEKNEQELLELDKWSLWNWF 36
Db 1 SLIHSLEESQIQEKNEQELLELDKWSLWNWF 34

RESULT 7
US-10-506-796A-1
; Sequence 1, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(35)
; OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)
US-10-506-796A-1

Query Match      69.8%; Score 134; DB 6; Length 35;
Best Local Similarity 96.0%; Pred. No. 5.2e-11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
Db 1 SQTQEKNEQELLELDKWSLWNWF 25

RESULT 8
US-10-506-796A-3
; Sequence 3, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafir
```

```
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-506-796A-3

Query Match      69.8%; Score 134; DB 6; Length 36;
Best Local Similarity 96.0%; Pred. No. 5.3e-11;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
Db 2 SQTQEKNEQELLELDKWSLWNWF 26

RESULT 9
US-10-841-956A-3
; Sequence 3, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-841-956A-3

Query Match      68.2%; Score 131; DB 6; Length 39;
Best Local Similarity 75.0%; Pred. No. 1.4e-10;
Matches 24; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 5 IYSLLEKSIQIQEKNEQELLELDKWSLWNWF 36
Db 8 ITALLEQAQIQEKNEQELYELQKLDKWSLWNWF 39

RESULT 10
US-11-029-003-3
; Sequence 3, Application US/11029003
; Publication No. US20050260194A1
; GENERAL INFORMATION:
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: RIVERA, DANIEL S.
; APPLICANT: BITONTI, ALAN J.
; APPLICANT: STATTEL, JAMES
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS
; FILE REFERENCE: 08945.0007-01000
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; CURRENT APPLICATION NUMBER: US/11/029,003
; CURRENT FILING DATE: 2005-01-05
; PRIOR APPLICATION NUMBER: 60/539,207
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: 60/487,964
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: 60/469,600
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent in ver. 3.2
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-11-029-003-3
Query Match 68.2%; Score 131; DB 7; Length 39;
Best Local Similarity 75.0%; Pred. No. 1.4e-10;
Matches 24; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 5 IYSLLEKSIQIQEKNEQELLELDKWSLWNWF 36
| : : : : : : : : : : : : : : : : : :
Db 8 ITALLEQAQIQEKNEVEYLQKLDKWSLWFW 39
| : : : : : : : : : : : : : : : : : :

RESULT 11
US-11-112-277-34
; Sequence 34, Application US/11112277
; Publication No. US20050267293A1
; GENERAL INFORMATION:
; APPLICANT: Bousquet-Gagnon, Nathalie
; APPLICANT: Quraishi, Omar
; APPLICANT: Bridon, Dominique P.
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN
; FILE REFERENCE: 500862003700
; CURRENT APPLICATION NUMBER: US/11/112,277
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/565,228
; PRIOR FILING DATE: 2004-04-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T1249 Analogue
; NAME/KEY: MOD_RES
; LOCATION: 40
; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA
US-11-112-277-34
Query Match 68.2%; Score 131; DB 7; Length 40;
Best Local Similarity 75.0%; Pred. No. 1.4e-10;
Matches 24; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 5 IYSLLEKSIQIQEKNEQELLELDKWSLWNWF 36
| : : : : : : : : : : : : : : : : : :
Db 8 ITALLEQAQIQEKNEVEYLQKLDKWSLWFW 39
| : : : : : : : : : : : : : : : : : :

RESULT 12
US-10-506-796A-7
; Sequence 7, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafirir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2

; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: HIV-1 isolate 1924v3.20 (residues 649-685)
US-10-506-796A-7
Query Match 67.2%; Score 129; DB 6; Length 36;
Best Local Similarity 92.0%; Pred. No. 2.3e-10;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
| : : : : : : : : : : : : : : : : : :
Db 1 SQNQEKNEQDLELDKWSLWNWF 25
| : : : : : : : : : : : : : : : : : :

RESULT 13
US-10-506-796A-5
; Sequence 5, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafirir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: HIV-1 isolate 593 clone (residues 649-685)
US-10-506-796A-5
Query Match 66.7%; Score 128; DB 6; Length 36;
Best Local Similarity 92.0%; Pred. No. 3.1e-10;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
| : : : : : : : : : : : : : : : : : :
Db 1 SQNQEKNEQELLELDKWSLWNWF 25
| : : : : : : : : : : : : : : : : : :

RESULT 14
US-10-506-796A-6
; Sequence 6, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafirir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
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; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(36)
; OTHER INFORMATION: HIV-1 isolate 98BRRS012 (residues 649-685)
US-10-506-796A-6
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Query Match          64.6%; Score 124; DB 6; Length 36;
Best Local Similarity 88.0%; Pred. No. 1e-09;
Matches 22; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 12 SQTQKEKNEQELLELDKWASLWNWF 36
Db 1 SQTQKEKNEHELELDKWANLWNWF 25
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```
RESULT 15
US-10-506-796A-4
; Sequence 4, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Tsafirir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(35)
; OTHER INFORMATION: HIV-1 isolate MN clone v5 (residues 649-685)
US-10-506-796A-4
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Query Match          63.5%; Score 122; DB 6; Length 36;
Best Local Similarity 88.0%; Pred. No. 1.8e-09;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 12 SQTQKEKNEQELLELDKWASLWNWF 36
Db 1 SQTQKEKNEQELLELDKWESLWNWF 25
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Job time : 10 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 16:12:57 ; Search time 117.333 Seconds  
(without alignments)  
134.809 Million cell updates/sec

Title: US-09-809-060A-4  
Perfect score: 36  
Sequence: 1 YTSLLYSLLKRSQIQKNEQELLELDKWSLWNP 36

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_21.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*
- 9: geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	100.0	36	3 AAY89840	Aay89840 Core poly
2	36	100.0	36	3 AAY89841	Aay89841 Core poly
3	36	100.0	36	4 AAB78242	Aab78242 Core poly
4	36	100.0	36	4 AAB78241	Aab78241 Core poly
5	36	100.0	36	4 AAB78241	Aab78241 Core poly
6	36	100.0	36	4 AAB78241	Aab78241 Core poly
7	36	100.0	36	4 ABB01248	Abb01248 Viral DP1
8	36	100.0	36	4 ABB01249	Abb01249 Viral DP1
9	36	100.0	36	4 ABB02833	Abb02833 Viral cor
10	36	100.0	36	4 AAU13794	Aau13794 DP178-lik
11	36	100.0	36	4 AAU13795	Aau13795 DP178-lik
12	36	100.0	36	5 AAC018774	Aac018774 HIV gp41
13	36	100.0	36	5 ADE02854	Ad02854 Hybrid po
14	36	100.0	36	5 ADE02853	Ad02853 Hybrid po
15	36	100.0	36	8 ADN06925	Adn06925 Peptide #
16	36	100.0	36	8 ADN06925	Adn06925 Peptide #
17	36	100.0	36	9 ADY71547	Ady71547 HIV-1 gp4
18	36	100.0	36	9 ADY71547	Ady71547 HIV-1 gp4
19	25	69.4	36	3 AAY89911	Aay89911 Core poly
20	25	69.4	36	4 AAB78312	Aab78312 Core poly
21	25	69.4	36	4 ABB01319	Abb01319 Viral DP1
22	25	69.4	36	4 AAU13865	Aau13865 DP178-lik
23	25	69.4	36	5 ADE02837	Ad02837 Hybrid po
24	25	69.4	268	2 AAY22811	Aay22811 SEQ ID NO

#### RESULT 1

AAy89840  
ID AAY89840 standard; peptide; 36 AA.  
XX  
AC AAY89840;  
XX  
DT 23-MAY-2000 (first entry)  
XX  
DE Core polypeptide fragment T No. 1409.  
XX  
KW Retrovirus; hybrid polypeptide; enhancer; gp41; envelope protein; HIV-1;  
KW HIV-2; SIV; pharmacokinetic; half-life; growth factor; cytokine; viral;  
KW anti-fusogenic; differentiation factor; interleukin; interferon;  
KW colony stimulating factor; hormone; angiogenic factor.  
XX  
OS Unidentified.  
XX  
PN WO9959615-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US011219.  
XX  
PR 20-MAY-1998; 98US-00082279.  
XX  
PA (TRIM-) TRIMERIS INC.  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX WPI; 2000-136792/12.  
XX  
PT A new hybrid polypeptide with enhanced pharmacokinetic properties  
XX comprises enhancer sequence.  
XX  
XX Disclosure; Page 45; 124pp; English.  
XX  
XX The invention relates to hybrid polypeptides comprising enhancer peptide  
XX sequence linked to core polypeptides. The enhancer polypeptides are  
XX derived from various retroviral envelope (gp41) protein sequences,  
XX especially from HIV-1, HIV-2 and SIV. The enhancer peptides enhance the  
XX pharmacokinetic properties such as increasing the half-life of any core  
XX polypeptide that they are linked to. The core polypeptides are any  
XX polypeptide that may be introduced into a living system and that can  
XX function as a pharmacologically useful peptide for the treatment or  
XX prevention of a disease. The core polypeptides are bioactive peptides  
XX selected from a growth factor, cytokine, differentiation factor,  
XX interleukin, interferon, colony stimulating factor, hormone or angiogenic

#### ALIGNMENTS

25	25	69.4	268	5	ABG68282	Abg68282 Envelope
26	25	69.4	268	6	ABU57689	Abu57689 Human imm
27	25	69.4	269	2	AY22825	SEQ ID NO
28	25	69.4	269	5	ABG68296	Abg68296 Envelope
29	25	69.4	269	6	ABU57703	Abu57703 Human imm
30	25	69.4	848	8	ADP20072	Adp20072 Human imm
31	25	69.4	848	9	ADP20072	Adp20072 Human imm
32	24	66.7	36	4	ABB02834	Abb02834 Viral cor
33	22	61.1	22	2	AAB14657	Aab14657 HIV-1 iso
34	22	61.1	22	3	AAB14657	Aab14657 HIV-1 iso
35	22	61.1	22	3	AAB52674	Aab52674 T20/DP178
36	22	61.1	22	3	AAB52699	Aab52699 T20/DP178
37	22	61.1	22	4	AAB54921	Aab54921 Anti-HIV
38	22	61.1	23	2	AAB64385	Aab64385 DP-178 ho
39	22	61.1	23	3	AAY88708	Aay88708 Core poly
40	22	61.1	23	3	AAB14658	Aab14658 HIV-1 iso
41	22	61.1	23	3	AAB52698	Aab52698 T20/DP178
42	22	61.1	23	3	AAB52675	Aab52675 T20/DP178
43	22	61.1	23	4	AAB54922	Aab54922 Anti-HIV
44	22	61.1	23	4	AAB77063	Aab77063 Core poly
45	22	61.1	23	4	ABB01532	Abb01532 Viral cor





```

XX DE Viral DP178/107-like region peptide T1409.
XX XX
XX OS
XX KW Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
XX KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
XX KW infection.
XX OS
XX XX
XX XX Viruses.
XX XX
XX XX Key Location/Qualifiers
XX FT Modified-site 1
XX FT Modified-site 36 /note= "N-terminal is substituted by Ac"
XX FT Modified-site 36 /note= "C-terminal amide"
XX XX
XX XX WO200164013-A2.
XX XX
XX PD 07-SEP-2001.
XX XX
XX XX 07-FEB-2001; 2001WO-US003988.
XX XX
XX XX 29-FEB-2000; 2000US-00515965.
XX XX
XX XX (TRIM-) TRIMERIS INC.
XX XX
XX XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX XX WPI; 2001-514829/56.
XX XX
XX XX Heptad repeat region peptide analogs useful for inhibiting virus/cells
XX XX fusion, useful for treating HIV and Respiratory Syncytial Virus
XX XX infection.
XX XX
XX XX Disclosure; Page 58; 587pp; English.
XX XX
XX XX The invention relates to isolated analogues of the heptad repeat region
XX XX peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
XX XX 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
XX XX respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
XX XX regions of proteins interact non-covalently with each other and/or with
XX XX peptides derived from them. This interaction is required for normal
XX XX infectivity of viruses such as RSV and HIV. The heptad repeat region
XX XX peptide analogues may be used to inhibit respiratory syncytial virus
XX XX (RSV) infection in a cell. They may also be used to inhibit HIV
XX XX infection. The present sequence is a peptide provided in the
XX XX specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
XX XX 11-SEP-2003 to standardise OS field)
XX XX
XX SQ Sequence 36 AA;
XX
XX Query Match 100.0%; Score 36; DB 4; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-25;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
XX | | | | | | | | | | | | | | | | | | | | | |
XX Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
XX
XX RESULT 7
XX ABB01249
XX ID ABB01249 standard; peptide; 36 AA.
XX XX
XX AC ABB01249;
XX XX
XX XX 11-SEP-2003 (revised)
XX DT 06-AUG-2003 (revised)
XX DT 03-JAN-2002 (first entry)
XX XX
XX XX Viral DP178/107-like region peptide T1410.
XX XX
XX XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
XX KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;

```

```

XX KW infection.
XX XX
XX OS Viruses.
XX XX
XX PN WO200164013-A2.
XX XX
XX XX PD 07-SEP-2001.
XX XX
XX XX 07-FEB-2001; 2001WO-US003988.
XX XX
XX PR 29-FEB-2000; 2000US-00515965.
XX XX
XX PA (TRIM-) TRIMERIS INC.
XX XX
XX PI Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;
XX XX WPI; 2001-514829/56.
XX XX
XX DR Heptad repeat region peptide analogs useful for inhibiting virus/cells
XX XX fusion, useful for treating HIV and Respiratory Syncytial Virus
XX XX infection.
XX XX
XX PS Disclosure; Page 58; 587pp; English.
XX XX
XX CC The invention relates to isolated analogues of the heptad repeat region
XX CC peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-
XX CC 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)
XX CC respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2
XX CC regions of proteins interact non-covalently with each other and/or with
XX CC peptides derived from them. This interaction is required for normal
XX CC infectivity of viruses such as RSV and HIV. The heptad repeat region
XX CC peptide analogues may be used to inhibit respiratory syncytial virus
XX CC (RSV) infection in a cell. They may also be used to inhibit HIV
XX CC infection. The present sequence is a peptide provided in the
XX CC specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on
XX CC 11-SEP-2003 to standardise OS field)
XX CC
XX SQ Sequence 36 AA;
XX
XX Query Match 100.0%; Score 36; DB 4; Length 36;
XX Best Local Similarity 100.0%; Pred. No. 4.2e-25;
XX Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
XX | | | | | | | | | | | | | | | | | | | | | |
XX Db 1 YTSLIYSLLEKSIQIQEKNEQELLELDKWASLWNWF 36
XX
XX RESULT 8
XX ABB02833
XX ID ABB02833 standard; peptide; 36 AA.
XX XX
XX AC ABB02833;
XX XX
XX DT 11-SEP-2003 (revised)
XX DT 06-AUG-2003 (revised)
XX DT 03-JAN-2002 (first entry)
XX XX
XX DE Viral core polypeptide, SEQ ID NO: 1360.
XX XX
XX XX Human immunodeficiency virus; HIV; respiratory syncytial virus; RSV;
XX KW virucide; heptad repeat region; transmembrane protein; gp41; HR1; HR2;
XX KW infection.
XX XX
XX OS Viruses.
XX XX
XX PN WO200164013-A2.
XX XX
XX PD 07-SEP-2001.
XX XX
XX PF 07-FEB-2001; 2001WO-US003988.
XX XX
XX PR 29-FEB-2000; 2000US-00515965.

```

XX (TRIM-) TRIMERIS INC.  
XX Antczak JB, Delmedico MK, Erickson JB, Lambert DM, Sista P;  
XX WPI; 2001-514829/56.  
XX  
XX Heptad repeat region peptide analogs useful for inhibiting virus/cells  
XX fusion, useful for treating HIV and Respiratory Syncytial Virus  
XX  
XX Disclosure; Page 525; 587pp; English.  
XX  
XX The invention relates to isolated analogues of the heptad repeat region  
XX peptides DP178 and DP107. DP178 and DP107 correspond to amino acids 638-  
XX 673 (heptad repeat region HR2) and 558-595 (heptad repeat region HR1)  
XX respectively, of HIV-1LAI transmembrane protein gp41. The HR1 and HR2  
XX regions of proteins interact non-covalently with each other and/or with  
XX peptides derived from them. This interaction is required for normal  
XX infectivity of viruses such as RSV and HIV. The heptad repeat region  
XX peptide analogues may be used to inhibit respiratory syncytial virus  
XX (RSV) infection in a cell. They may also be used to inhibit HIV  
XX infection. The present sequence is a peptide provided in the  
XX specification. (Updated on 06-AUG-2003 to correct OS field.) (Updated on  
XX 11-SEP-2003 to standardise OS field)  
XX  
SQ Sequence 36 AA;  
Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.2e-25;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YTSIIYSLLSKSQIQEKNEQELLELDKQASLWNWF 36  
Db 1 YTSIIYSLLSKSQIQEKNEQELLELDKQASLWNWF 36  
RESULT 9  
AAU13794  
ID AAU13794 standard; peptide; 36 AA.  
XX  
XX AAU13794;  
XX  
XX 21-NOV-2001 (first entry)  
XX  
XX DP178-like/DP107-like peptide T-1409.  
XX  
XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
XX antifusogenic; antiviral; HIV transmission; mutant; mutein.  
XX  
XX Human immunodeficiency virus 1; isolate LAI.  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
XX Modified-site 1  
XX FT /note= "N-terminal is substituted by Ac"  
XX Modified-site 36  
XX FT /note= "C-terminal amide"  
XX  
XX WO200151673-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JUL-2000; 2000WO-US035727.  
XX  
XX 09-JUL-1999; 99US-00350841.  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
XX WPI; 2001-442157/47.  
XX

PT Identifying a compound that inhibits the formation of or disrupts a  
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
PT or intracellular modulatory activity, by detecting the formation of a  
XX DP107/DP178 complex.  
XX Disclosure; Page 77; 259pp; English.  
XX  
XX The present invention relates to peptides which exhibit anti-retroviral  
XX activity. The peptides of the invention (AAU12559-AAU14009) comprise  
XX DP178-like and DP107-like peptides. The DP178 peptide corresponds to  
XX amino acids 639-673 of the transmembrane protein gp41 from human  
XX immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
XX corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
XX also relates to a method of identifying compounds that inhibit the  
XX formation of or disrupts a DP107/DP178 complex. The method comprises  
XX detecting the formation of a DP107/DP178 complex, both in the presence or  
XX absence of a test compound, in a reaction mixture containing DP107 and  
XX DP178 peptides. The method is useful for identifying compounds, including  
XX small molecule compounds, which may themselves exhibit antifusogenic,  
XX antiviral or intracellular modulatory activity. The DP178-like/DP107-like  
XX peptides are useful to inhibit human and non-human retroviral,  
XX particularly HIV, transmission to uninfected cells. The present sequence  
XX represents one of the DP178-like/DP107-like peptides of the invention  
XX  
SQ Sequence 36 AA;  
Query Match 100.0%; Score 36; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.2e-25;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YTSIIYSLLSKSQIQEKNEQELLELDKQASLWNWF 36  
Db 1 YTSIIYSLLSKSQIQEKNEQELLELDKQASLWNWF 36  
RESULT 10  
AAU13795  
ID AAU13795 standard; peptide; 36 AA.  
XX  
XX AAU13795;  
XX  
XX 21-NOV-2001 (first entry)  
XX  
XX DP178-like/DP107-like peptide T-1410.  
XX  
XX Anti-retroviral; DP178-like; DP107-like; transmembrane protein gp41;  
XX antifusogenic; antiviral; HIV transmission; mutant; mutein.  
XX  
XX Human immunodeficiency virus 1; isolate LAI.  
XX Synthetic.  
XX  
XX WO200151673-A2.  
XX  
XX 19-JUL-2001.  
XX  
XX 05-JUL-2000; 2000WO-US035727.  
XX  
XX 09-JUL-1999; 99US-00350841.  
XX (TRIM-) TRIMERIS INC.  
XX  
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;  
XX WPI; 2001-442157/47.  
XX  
XX Identifying a compound that inhibits the formation of or disrupts a  
XX DP107/DP178 complex, especially compounds with antifusogenic, antiviral  
XX or intracellular modulatory activity, by detecting the formation of a  
XX DP107/DP178 complex.  
XX Disclosure; Page 77; 259pp; English.  
XX  
XX The present invention relates to peptides which exhibit anti-retroviral

CC activity. The peptides of the invention (AAU12559-AAU14009) comprise  
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to  
 CC amino acids 639-673 of the transmembrane protein gp41 from human  
 CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide  
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention  
 CC also relates to a method of identifying compounds that inhibit the  
 CC formation of or disrupts a DP107/DP178 complex. The method comprises  
 CC detecting the formation of a DP107/DP178 complex, both in the presence or  
 CC absence of a test compound, in a reaction mixture containing DP107 and  
 CC DP178 peptides. The method is useful for identifying compounds, including  
 CC small molecule compounds, which may themselves exhibit antifusogenic,  
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like  
 CC peptides are useful to inhibit human and non-human retroviral,  
 CC particularly HIV, transmission to uninfected cells. The present sequence  
 CC represents one of the DP178-like/DP107-like peptides of the invention  
 XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 4; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-25;  
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36  
 |||||  
 Db 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

## RESULT 11

AAO18774  
 ID AAO18774 standard; peptide; 36 AA.

AC AAO18774;

XX 29-OCT-2002 (first entry)

DE HIV gp41 protein DP-178 region derived peptide SEQ ID NO: 5.

XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;  
 KW gp41.

XX Human immunodeficiency virus.

OS WO200256902-A2.

XX 25-JUL-2002.

XX 17-DEC-2001; 2001WO-US048802.

XX 19-DEC-2000; 2000US-0256657P.

XX (SCHE ) SCHERING CORP.

XX Baroudy BM;

XX WPI; 2002-636513/68.

XX Treatment of HIV infection in an individual involves administration of a  
 PT combination of chemokine co-receptor five antagonist and a specified HIV  
 PT envelope polypeptide.

XX Disclosure; Page 32; 52pp; English.

XX The present invention relates to a method of treating an HIV infection in  
 CC an individual, which involves administering in combination a chemokine co  
 CC -receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its  
 CC derivative. Other viral infections can also be treated using the method.  
 CC The present sequence is a peptide derived from HIV and useful in the  
 CC method of the invention

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 5; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-25;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36  
 |||||  
 Db 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

## RESULT 12

AAO18826  
 ID AAO18826 standard; peptide; 36 AA.

XX AAO18826;

XX 29-OCT-2002 (first entry)

DE HIV gp41 protein DP-178 region derived peptide SEQ ID NO: 57.

XX Viral infection; HIV; antiviral; DP-178; CCR5 antagonist; T-20; DP-107;  
 KW gp41.

XX Human immunodeficiency virus.

XX WO200256902-A2.

XX 25-JUL-2002.

XX 17-DEC-2001; 2001WO-US048802.

XX 19-DEC-2000; 2000US-0256657P.

XX (SCHE ) SCHERING CORP.

XX Baroudy BM;

XX WPI; 2002-636513/68.

XX Treatment of HIV infection in an individual involves administration of a  
 PT combination of chemokine co-receptor five antagonist and a specified HIV  
 PT envelope polypeptide.

XX Disclosure; Page 34; 52pp; English.

XX The present invention relates to a method of treating an HIV infection in  
 CC an individual, which involves administering in combination a chemokine co  
 CC -receptor 5 (CCR5) antagonist or its salt and a DP-178 polypeptide or its  
 CC derivative. Other viral infections can also be treated using the method.  
 CC The present sequence is a peptide derived from HIV and useful in the  
 CC method of the invention

XX Sequence 36 AA;

Query Match 100.0%; Score 36; DB 5; Length 36;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-25;

Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36  
 |||||  
 Db 1 YTSIIYSLLEKSQIQQEKNEQELLELDKWASLWNWF 36

## RESULT 13

ADE02854  
 ID ADE02854 standard; peptide; 36 AA.

XX ADE02854;

XX 29-JAN-2004 (first entry)

DE Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID NO 1361.

XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;  
 KW pharmacokinetic; fusogenic; insulin; diabetes.

OS Unidentified.  
XX US6348568-B1.  
XX  
XX  
PD 19-FEB-2002.  
XX  
XX 20-MAY-1999; 99US-00315304.  
XX  
XX 20-MAY-1998; 98US-00082279.  
PR  
XX (TRIM-) TRIMERIS INC.  
XX  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
XX WPI; 2002-424396/45.  
XX  
XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral  
PT activity, has enhancer peptide sequence derived from retroviral envelope  
PT protein sequences linked to core polypeptide e.g. therapeutic protein.  
XX  
XX Disclosure; SEQ ID NO 1361; 70pp; English.  
XX  
XX The invention relates to a novel hybrid polypeptide comprising an  
CC enhancer peptide sequence linked to a core polypeptide. The enhancer  
CC peptide sequence comprises WQWEQKI or WASLWFW. The invention also  
CC includes novel peptides that exhibit anti-fusogenic activity, antiviral  
CC activity and/or ability to modulate intracellular processes. The novel  
CC hybrid polypeptide has virucide and antidiabetic activity. The enhancer  
CC peptide sequence enhances pharmacokinetic properties of any core  
CC polypeptide, for example, a polypeptide useful for the treatment or  
CC prevention of a disease, or an imaging agent useful for imaging  
CC structures in vivo. The core polypeptides and hybrid polypeptides are  
CC useful for modulating fusogenic events and exhibit antifusogenic or  
CC antiviral activity. The novel hybrid polypeptide is useful for decreasing  
CC viral infection and modulating intracellular processes involving coiled-  
CC coil peptide interactions. The novel hybrid polypeptide comprises insulin  
CC or its fragment, so the core polypeptide is useful for ameliorating the  
CC symptoms of forms of diabetes. The novel hybrid polypeptide is also  
CC useful as a part of prognosis for preventing disorders including fusion  
CC events and viral infection that involves cell-cell and/or virus-cell  
CC fusion, and for diagnosis and in vivo imaging methods. This sequence  
CC represents an enhancer peptide of the invention.  
XX  
SQ Sequence 36 AA;  
Query Match 100.0%; Score 36; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.2e-25;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YTSLIYSLLKSKIQQEKNEQELLELDKWASLWNWF 36  
Db 1 YTSLIYSLLKSKIQQEKNEQELLELDKWASLWNWF 36  
RESULT 14  
ADE02853  
ID ADE02853 standard; peptide; 36 AA.  
XX  
XX ADE02853;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX Hybrid polypeptide pharmacokinetic enhancer peptide, SEQ ID NO 1360.  
XX  
XX hybrid; enhancer; anti-fusogenic; antiviral; virucide; antidiabetic;  
KW pharmacokinetic; fusogenic; insulin; diabetes.  
XX  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
FH Modified-site 1  
FT /note= "Residue is modified by acetyl group"  
FT Modified-site 36

/note= "C-terminal amide"  
FT US6348568-B1.  
XX  
XX  
XX 19-FEB-2002.  
XX  
XX 20-MAY-1999; 99US-00315304.  
XX  
XX 20-MAY-1998; 98US-00082279.  
PR  
XX (TRIM-) TRIMERIS INC.  
XX  
XX  
PI Barney S, Guthrie KI, Merutka G, Anwer MK, Lambert DM;  
XX  
XX WPI; 2002-424396/45.  
XX  
XX New hybrid polypeptide for modulating fusogenic events for e.g. antiviral  
PT activity, has enhancer peptide sequence derived from retroviral envelope  
PT protein sequences linked to core polypeptide e.g. therapeutic protein.  
XX  
XX Disclosure; SEQ ID NO 1360; 70pp; English.  
XX  
XX The invention relates to a novel hybrid polypeptide comprising an  
CC enhancer peptide sequence linked to a core polypeptide. The enhancer  
CC peptide sequence comprises WQWEQKI or WASLWFW. The invention also  
CC includes novel peptides that exhibit anti-fusogenic activity, antiviral  
CC activity and/or ability to modulate intracellular processes. The novel  
CC hybrid polypeptide has virucide and antidiabetic activity. The enhancer  
CC peptide sequence enhances pharmacokinetic properties of any core  
CC polypeptide, for example, a polypeptide useful for the treatment or  
CC prevention of a disease, or an imaging agent useful for imaging  
CC structures in vivo. The core polypeptides and hybrid polypeptides are  
CC useful for modulating fusogenic events and exhibit antifusogenic or  
CC antiviral activity. The novel hybrid polypeptide is useful for decreasing  
CC viral infection and modulating intracellular processes involving coiled-  
CC coil peptide interactions. The novel hybrid polypeptide comprises insulin  
CC or its fragment, so the core polypeptide is useful for ameliorating the  
CC symptoms of forms of diabetes. The novel hybrid polypeptide is also  
CC useful as a part of prognosis for preventing disorders including fusion  
CC events and viral infection that involves cell-cell and/or virus-cell  
CC fusion, and for diagnosis and in vivo imaging methods. This sequence  
CC represents an enhancer peptide of the invention.  
XX  
SQ Sequence 36 AA;  
Query Match 100.0%; Score 36; DB 5; Length 36;  
Best Local Similarity 100.0%; Pred. No. 4.2e-25;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 YTSLIYSLLKSKIQQEKNEQELLELDKWASLWNWF 36  
Db 1 YTSLIYSLLKSKIQQEKNEQELLELDKWASLWNWF 36  
RESULT 15  
ADN06925  
ID ADN06925 standard; protein; 36 AA.  
XX  
XX ADN06925;  
XX  
XX 17-JUN-2004 (first entry)  
XX  
XX Peptide #36 used in the pharmaceutical composition of the invention.  
XX  
XX Pharmaceutical; human immunodeficiency virus; HIV; gp41; glycoprotein41;  
KW HIV infection; antiviral; therapy.  
XX  
XX Unidentified.  
XX  
XX US2004063637-A1.  
XX  
XX 01-APR-2004.  
XX





GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:19:28 ; Search time 19 Seconds  
(without alignments)  
182.305 Million cell updates/sec

Title: US-09-809-060A-4  
Perfect score: 36  
Sequence: 1 YTSLLVLEKSQIQEKNEQELLELDKWASLWNWP 36

Scoring table:  
OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	61.1	357	2 S21994	envelope protein g
2	22	61.1	357	2 S21996	envelope protein g
3	22	61.1	358	2 S21998	envelope protein g
4	22	61.1	443	2 C41621	env polypeptide P
5	22	61.1	847	2 T09448	envelope glycoprotein
6	22	61.1	847	2 S13289	env protein - huma
7	22	61.1	851	2 S33985	env polypeptide -
8	22	61.1	853	2 S54384	envelope polypeptide
9	22	61.1	854	2 S13288	env protein - huma
10	22	61.1	855	1 VCLJ32	env polypeptide pr
11	22	61.1	855	1 VCLJ2R	env polypeptide pr
12	22	61.1	856	1 VCLJ3W	env polypeptide pr
13	22	61.1	856	1 VCLJH3	env polypeptide pr
14	22	61.1	859	1 VCLJWN	env polypeptide pr
15	22	61.1	861	1 VCLJSC	env polypeptide pr
16	22	61.1	861	1 VCLJVV	env polypeptide pr
17	19	52.8	357	2 S21992	envelope protein g
18	16	44.4	852	2 T12016	envelope glycoprotein
19	16	44.4	856	1 VCLJVL	env polypeptide pr
20	15	41.7	846	1 VCLJND	env polypeptide pr
21	15	41.7	852	1 VCLJBR	env polypeptide -
22	15	41.7	859	2 T01672	envelope polypeptide
23	11	30.6	445	2 A41621	env polypeptide M
24	11	30.6	843	1 H44001	env polypeptide pr
25	10	27.8	357	2 S22004	envelope protein g
26	10	27.8	357	2 S22006	envelope protein g
27	10	27.8	357	2 S21990	envelope protein g
28	8	22.2	454	2 B41621	env polypeptide D
29	8	22.2	592	2 T03682	catechol oxidase (

30 catechol oxidase (

31 catechol oxidase (

32 env polypeptide pr

33 env polypeptide -

34 envelope polypeptide

35 envelope polypeptide

36 env protein - huma

37 env protein - huma

38 env protein - huma

39 env protein - huma

40 env protein - huma

41 env protein - huma

42 env protein - huma

43 env protein - huma

44 env protein - huma

45 env protein - huma

## ALIGNMENTS

## RESULT 1

S21994  
envelope protein gp120/gp41 - human immunodeficiency virus type 1

C;Species: human immunodeficiency virus type 1, HIV-1

A;Variety: isolate 27B

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S21994; S70421

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

submitted to the EMBL Data Library, July 1991

A;Description: Distinct populations of HIV-1 in blood and cerebrospinal fluid as determined

A;Reference number: S21990

A;Accession: S21994

A;Molecule type: DNA

A;Residues: 1-357 <ST2>

A;Cross-references: UNIPROT:Q78118; UNIPARC:UPI0000178606; EMBL:X61355; NID:G60179; PIDN

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A;Reference number: S70417; MUID:92144209; PMID:1736940

A;Accession: S70421

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-140, 'X', 142-312, 'X', 314-357 <STE2>

A;Cross-references: UNIPARC:UPI00000FF05F; EMBL:X61355; NID:G60179

C;Superfamily: type E retrovirus env polypeptide

Query Match 61.1%; Score 22; DB 2; Length 357;  
Best Local Similarity 100.0%; Pred. No. 4.6e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKWASLWNWP 36

Db 153 QQEKNEQELLELDKWASLWNWP 174

## RESULT 2

S21996

envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 27L)

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S70422; S21996

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebro

A;Reference number: S70417; MUID:92144209; PMID:1736940

A;Accession: S70422

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-357 <ST2>

A;Cross-references: UNIPROT:Q78118; UNIPARC:UPI00000104EC6; EMBL:X61355; NID:G60181; PIDN

A;Experimental source: patient 27L

A;Note: submitted to the EMBL Data Library, July 1991



A:Molecule type: mRNA  
A:Residues: 1-851 <CR>  
A:CROSS-references: UNIPROT:Q78243; UNIPARC:UPI00001067CD; EMBL:Z11530; NID:G60192; PIDN  
C:Superfamily: type E retrovirus env polyprotein

Query Match 61.1%; Score 22; DB 2; Length 851;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKQASLWNNWF 36  
Db 647 QQEKNEQELLELDKQASLWNNWF 668

RESULT 8  
S54384  
envelope polyprotein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 09-Jul-2004  
C:Accession: S54384  
R:Theodore, T.; Buckler-White, A.J.  
submitted to the EMBL Data Library, July 1989  
A:Reference number: S54377  
A:Accession: S54384  
A>Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-853 <THE>  
A:CROSS-references: UNIPROT:P12487; UNIPARC:UPI000012A027; EMBL:M22639; NID:G329377; PID  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: polyprotein

Query Match 61.1%; Score 22; DB 2; Length 853;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKQASLWNNWF 36  
Db 649 QQEKNEQELLELDKQASLWNNWF 670

RESULT 9  
S13288  
env protein - human immunodeficiency virus type 1  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Dec-2004  
C:Accession: S13288  
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Digne, A.; Idler, K.; Zack, J.A  
Nature 348, 69-73, 1990  
A>Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120  
A:Reference number: S13288; MUID:91043044; PMID:2172833  
A:Accession: S13288  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-854 <OR>  
A:CROSS-references: UNIPROT:Q85582; UNIPROT:Q72502; UNIPROT:Q90178; UNIPROT:Q78243; UNIP

Query Match 61.1%; Score 22; DB 2; Length 854;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKQASLWNNWF 36  
Db 650 QQEKNEQELLELDKQASLWNNWF 671

RESULT 10  
VCLJ3W  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate ARV-2)  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus type 1, HIV-1  
A>Note: host Homo sapiens (man)  
C>Date: 17-May-1985 #sequence\_revision 17-May-1985 #text\_change 09-Jul-2004  
C:Accession: A03976

R:Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Stempien, M.M.; Brown-Sh  
Science 227, 484-492, 1985  
A>Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).  
A:Reference number: A04003; MUID:85090453; PMID:2578227  
A:Accession: A03976  
A:Molecule type: DNA  
A:Residues: 1-855 <SAN>  
A:CROSS-references: UNIPROT:P03378; UNIPARC:UPI000012A00F; GB:K02007; NID:G328658; PIDN:  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
F:1-30/Domain: signal sequence #status predicted <SIG>  
F:31-509/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:510-855/Product: transmembrane glycoprotein #status predicted <TMM>  
F:87,129,140,158,184,190,200,244,265,292,298,304,334,341,358,364,388,394,400,408,445,458  
F:610,624,636,815/Binding site: carbohydrate (Aan) (covalent) #status predicted  
Query Match 61.1%; Score 22; DB 1; Length 855;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKQASLWNNWF 36  
Db 651 QQEKNEQELLELDKQASLWNNWF 672

RESULT 11  
VCLJ3R  
env polyprotein precursor - human immunodeficiency virus Zr-6  
N:Alternate names: coat polyprotein  
C:Species: human immunodeficiency virus Zr-6  
C>Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
C:Accession: D26192  
R:Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu  
Gene 52, 71-82, 1987  
A>Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti  
A:Reference number: A26192; MUID:87248097; PMID:3036660  
A:Accession: D26192  
A:Molecule type: DNA  
A:Residues: 1-855 <SRI>  
A:CROSS-references: UNIPROT:P04580; UNIPARC:UPI000012A029; GB:K03458; NID:G32  
C:Genetics:  
A:Gene: env  
C:Superfamily: type E retrovirus env polyprotein  
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-855/Product: env polyprotein #status predicted <MAT>  
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>  
F:501-855/Product: transmembrane glycoprotein #status predicted <TMM>  
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404  
Query Match 61.1%; Score 22; DB 1; Length 855;  
Best Local Similarity 100.0%; Pred. No. 1e-13;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKQASLWNNWF 36  
Db 651 QQEKNEQELLELDKQASLWNNWF 672

RESULT 12  
VCLJ3W  
env polyprotein precursor - human immunodeficiency virus type 1 (isolate WMJ1)  
N:Contains: coat protein gp120; coat protein gp41  
C:Species: human immunodeficiency virus type 1, HIV-1  
C>Date: 30-Sep-1988 #sequence\_revision 30-Sep-1988 #text\_change 09-Jul-2004  
C:Accession: A24774  
R:Starcich, B.R.; Hahn, B.H.; Shaw, G.M.; McNeely, P.D.; Modrow, S.; Wolf, H.; Parks, E.  
Cell 45, 637-648, 1986  
A>Title: Identification and characterization of conserved and variable regions in the en  
A:Reference number: A24774; MUID:86218077; PMID:2423250  
A:Accession: A24774

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A:Molecule type: DNA
A:Residues: 1-856 <STA>
A:Cross-references: UNIPROT:P31872; UNIPARC:UPI000012A024; GB:M38432; NID:G19
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <GPI>
F:502-847/Product: coat protein gp41 #status predicted <GP2>
F:87,134,140,151,155,183,197,234,241,262,276,289,295,331,338,354,360,390,394,404,447,459
Query Match 61.1%; Score 22; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 652 QOEKNEQELLELDKWASLWNWF 673
RESULT 13
VCLJH3
env polypeptide precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora-
nberger, J.A.; Papas, T.S.; Grzyb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:8511123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: UNIPROT:P03375; UNIPARC:UPI000012A010; GB:M15654; GB:K02008; GB:K020
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polypept
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-511/Product: exterior membrane glycoprotein #status predicted <EXT>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMW>
F:88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predic
Query Match 61.1%; Score 22; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 652 QOEKNEQELLELDKWASLWNWF 673
RESULT 14
VCLJMN
env polypeptide precursor - human immunodeficiency virus type 1 (isolate MN)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: A28922
R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
Virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: A28922
A:Molecule type: DNA
A:Residues: 1-859 <GUR>
A:Cross-references: UNIPARC:UPI0000174A38
```

```
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-859/Product: env polypeptide #status predicted <PPP>
F:87,129,135,140,141,146,161,165,191,202,246,267,281,294,300,336,343,359,365,389,395,401
Query Match 61.1%; Score 22; DB 1; Length 859;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 656 QOEKNEQELLELDKWASLWNWF 677
RESULT 15
VCLJSC
env polypeptide precursor - human immunodeficiency virus type 1 (isolate SC)
N:Alternate names: coat polypeptide
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Feb-1997
C:Accession: B28922
R:Gurgo, C.; Guo, H.G.; Franchini, G.; Aldovini, A.; Collalti, E.; Farrell, K.; Wong-Sta
Virology 164, 531-536, 1988
A:Title: Envelope sequences of two new United States HIV-1 isolates.
A:Reference number: A28922; MUID:88219542; PMID:3369091
A:Accession: B28922
A:Molecule type: DNA
A:Residues: 1-861 <GUR>
A:Cross-references: UNIPARC:UPI0000174A39
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polypeptide
C:Keywords: capsid protein; coat protein; glycoprotein; polypeptide; transmembrane prote
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-861/Product: env polypeptide #status predicted <PPP>
F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396
Query Match 61.1%; Score 22; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 1e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 15 QOEKNEQELLELDKWASLWNWF 36
Db 657 QOEKNEQELLELDKWASLWNWF 678
Search completed: March 6, 2006, 16:26:19
Job time : 19 secs
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 6, 2006, 16:13:17 ; Search time 122 Seconds  
(without alignments)  
208.189 Million cell updates/sec

Title: US-09-809-060A-4  
Perfect score: 36  
Sequence: 1 YTSLLYSLEKSIQOEKNEQELLELDKWSLWNWF 36

Scoring table:  
Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	80.6	121	2 Q6WH74	human immun
2	29	80.6	122	2 Q6EA81	human immun
3	29	80.6	122	2 Q9YXQ1	human immun
4	27	75.0	122	2 Q6DL64	human immun
5	27	75.0	128	2 Q6JEV9	human immun
6	27	75.0	145	2 Q7ZCS5	human immun
7	27	75.0	146	2 Q6JFV9	human immun
8	27	75.0	867	2 Q7ZC00	human immun
9	27	75.0	868	2 Q7ZC01	human immun
10	26	72.2	126	2 Q6V908	human immun
11	25	69.4	34	2 Q69893	human immun
12	25	69.4	49	2 Q69895	human immun
13	25	69.4	49	2 Q69896	human immun
14	25	69.4	118	2 Q6E583	human immun
15	25	69.4	121	2 Q6WH14	human immun
16	25	69.4	122	2 Q6WG09	human immun
17	25	69.4	122	2 Q6WH11	human immun
18	25	69.4	122	2 Q6DL06	human immun
19	25	69.4	122	2 Q6DL34	human immun
20	25	69.4	122	2 Q6DL40	human immun
21	25	69.4	122	2 Q6EA80	human immun
22	25	69.4	125	2 Q6V900	human immun
23	25	69.4	130	2 Q6V823	human immun
24	25	69.4	142	2 Q6JFE1	human immun
25	25	69.4	144	2 Q7ZC91	human immun
26	25	69.4	144	2 Q6JFJ2	human immun
27	25	69.4	724	2 Q6QKH4	human immun
28	25	69.4	831	2 Q6S516	human immun
29	25	69.4	848	1 ENV HV1JR	human immun
30	25	69.4	848	2 Q6BC22	human immun
31	25	69.4	848	2 Q6TAN0	human immun

32	25	69.4	848	2 Q6TAN1	9HIV1	Q6tan1 human immun
33	25	69.4	848	2 Q6TAN2	9HIV1	Q6tan2 human immun
34	25	69.4	848	2 Q74999	9HIV1	Q74999 human immun
35	25	69.4	850	2 Q79795	9HIV1	Q79795 human immun
36	25	69.4	855	2 Q902H5	9HIV1	Q902h5 human immun
37	25	69.4	860	2 Q41532	9HIV1	Q41532 human immun
38	25	69.4	868	2 Q8Q861	9HIV1	Q8q861 human immun
39	22	61.1	34	2 Q69894	9HIV1	Q69894 human immun
40	22	61.1	34	2 Q69905	9HIV1	Q69905 human immun
41	22	61.1	42	2 Q69910	9HIV1	Q69910 human immun
42	22	61.1	49	2 Q69909	9HIV1	Q69909 human immun
43	22	61.1	117	2 Q6WH02	9HIV1	Q6wh02 human immun
44	22	61.1	117	2 Q6WH53	9HIV1	Q6wh53 human immun
45	22	61.1	117	2 Q6WH80	9HIV1	Q6wh80 human immun

#### ALIGNMENTS

RESULT 1  
Q6WH74\_9HIV1  
ID Q6WH74\_9HIV1 PRELIMINARY; PRT; 121 AA.  
AC Q6WH74;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Envelope glycoprotein (Fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Lentivirus; Primate lentivirus group.  
OX NCBI\_TaxID=11676;  
RN NUCLEOTIDE SEQUENCE.  
RP PubMed=14715797; DOI=10.1128/JCM.42.1.426-430.2004;  
RX Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,  
RA Gouvea M.I.F.S., Guimaraes M.A.A.M., De Oliveira F.E.,  
RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;  
RT "Prevalence of human immunodeficiency virus drug resistance mutations  
and subtypes in drug-naive, infected individuals in the army health  
RT service of Rio de Janeiro, Brazil."  
RL J. Clin. Microbiol. 42:426-430(2004).  
DR EMBL; AY285022; AAQ68085.1; -; Genomic RNA.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0019031; C:viral envelope; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR000328; Env\_Gp41.  
DR Pfam; PF00517; GP41; 1.  
KW Envelope protein.  
FT NON\_TER 1 121  
FT NON\_TER 121 121  
SQ SEQUENCE 121 AA; 14738 MW; 65B8CB4D6200BFAF CRC64;  
Query Match 80.6%; Score 29; DB 2; Length 121;  
Best Local Similarity 100.0%; Pred.No. 6.9e-20;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 8 LLEKSIQOEKNEQELLELDKWSLWNWF 36  
Db 84 LLEKSIQOEKNEQELLELDKWSLWNWF 112  
RESULT 2  
Q6EA81\_9HIV1  
ID Q6EA81\_9HIV1 PRELIMINARY; PRT; 122 AA.  
AC Q6EA81;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Envelope glycoprotein (fragment).  
GN Name=env;  
OS Human immunodeficiency virus 1.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;

```

OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BX923;
RX MEDLINE=20134570; PubMed=10669328; DOI=10.1086/315253;
RA Weidle P.J., Ganea C.E., Irwin K.L., Pieniazek D., McGowan J.P.,
RA Olivo N., Ramos A., Schable C., Lal R.B., Holmberg S.D., Ernst J.A.;
RT "Presence of human immunodeficiency virus (HIV) type 1, group M, non-B
RT subtypes, Bronx, New York: a sentinel site for monitoring HIV genetic
RT diversity in the United States.";
RL J. Infect. Dis. 181:470-475 (2000).
DR EMBL; AF190971; AAG02333.1; -; Genomic_DNA.
DR HSSP; P12488; 11W7.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
KW Name=env;
KW NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14753 MW; C3FE4DB1F8B5BCBD CRC64;

Query Match 80.6%; Score 29; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.9e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LLEKSIQOEKNEQELLELDKWSLWNWF 36
Db 85 LLEKSIQOEKNEQELLELDKWSLWNWF 113

RESULT 3
Q9YXQ1_9HIV1
ID Q9YXQ1_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q9YXQ1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein immunodominant region (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99125811; PubMed=9928731;
RA Tanuri A., Swanson P., Devare S., Berro O.J., Savedra A., Costa L.J.,
RA Telles J.G., Brindeiro R., Schable C., Pieniazek D., Rayfield M.;
RT "HIV-1 subtypes among blood donors from Rio de Janeiro, Brazil.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 20:60-66 (1999).
DR EMBL; AF034052; AAC79304.1; -; Genomic_RNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
KW NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14792 MW; 705BB60146B8FD17 CRC64;

Query Match 80.6%; Score 29; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 6.9e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 LLEKSIQOEKNEQELLELDKWSLWNWF 36
Db 85 LLEKSIQOEKNEQELLELDKWSLWNWF 113

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RESULT 4
Q6DL64_9HIV1
ID Q6DL64_9HIV1 PRELIMINARY; PRT; 122 AA.
AC Q6DL64;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Kalish M.L., Robbins K.E., Pieniazek D., Schaefer A., Nzilambi N.,
RA Quinn T.C., StLouis M.E., Youngpairoj A.S., Phillips J., Jaffe H.W.,
RA Folks T.M.;
RT "Recombinant viruses and early global HIV-1 epidemic.";
RL Emerg. Infect. Dis. 10:1227-1234 (2004).
DR EMBL; AY667639; AAT74945.1; -; Genomic_DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
KW NON_TER 1 1
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 14800 MW; 862308FF35EB4A3F CRC64;

Query Match 75.0%; Score 27; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 5.7e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 EKSOIQOEKNEQELLELDKWSLWNWF 36
Db 87 EKSOIQOEKNEQELLELDKWSLWNWF 113

RESULT 5
Q6JEV9_9HIV1
ID Q6JEV9_9HIV1 PRELIMINARY; PRT; 128 AA.
AC Q6JEV9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Yang C., Li M., Shi Y.P., Winter J., van Bijk A.M., Ayisi J., Hu D.J.,
RA Steketee R., Nahlen B.L., Lal R.B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY493156; AAT05980.1; -; Genomic_RNA.
DR SMR; O6JEV9; 1-74.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
KW NON_TER 1 1
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 15494 MW; 807346D5E52C194 CRC64;

Query Match 75.0%; Score 27; DB 2; Length 128;
Best Local Similarity 100.0%; Pred. No. 5.9e-18;

```

```
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 EKSQIQEKNEQELLELDKWSLWNWF 36
Db 95 EKSQIQEKNEQELLELDKWSLWNWF 121

RESULT 6
Q7ZC55_9HIV1 PRELIMINARY; PRT; 145 AA.
AC Q7ZC55;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE Envelope glycoprotein (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22679027; PubMed=12794544;
RX DOI=10.1097/00126334-200306010-00003;
RA Roman F., Gonzalez D., Lambert C., Deroo S., Fischer A., Baurith T.,
RA Staub T., Boulme R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.,
RT "Uncommon mutations at residue positions critical for enfuvirtide (T-
RT 20) resistance in enfuvirtide-naïve patients infected with subtype B
RT and non-B HIV-1 strains."
RL J. Acquir. Immune Defic. Syndr. 33:134-139(2003).
DR EMBL; AY185465; AA065740.1; -; Genomic_RNA.
DR HSSP; P04578; 1DLB.
DR SMR; Q7ZC55; 9-92.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
DR KW Envelope protein.
FT NON_TER 1
FT TER 145
SQ SEQUENCE 145 AA; 16928 MW; D72B68F6A0812805 CRC64;

Query Match 75.0%; Score 27; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 6.6e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 EKSQIQEKNEQELLELDKWSLWNWF 36
Db 116 EKSQIQEKNEQELLELDKWSLWNWF 142

RESULT 7
Q6JFV9_9HIV1 PRELIMINARY; PRT; 146 AA.
AC Q6JFV9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Envelope glycoprotein (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Yang C., Li M., Shi Y.P., Winter J., van Eijk A.M., Ayisi J., Hu D.J.,
RA Steketee R., Nahlen B.L., Lal R.B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY492806; AAT05630.1; -; Genomic_RNA.
DR HSSP; P04578; 1K33.
DR SMR; Q6JFV9; 1-82.
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DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT TER 146
SQ SEQUENCE 146 AA; 17524 MW; 642595EF4695BB02 CRC64;

Query Match 75.0%; Score 27; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 6.6e-18;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 EKSQIQEKNEQELLELDKWSLWNWF 36
Db 103 EKSQIQEKNEQELLELDKWSLWNWF 129

RESULT 8
Q7ZC00_9HIV1 PRELIMINARY; PRT; 867 AA.
AC Q7ZC00;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE Envelope glycoprotein.
GN Name=gp160;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Daniela R.S., Wilson P., Patel D., Longhurst H., Patterson S.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AJ535609; CAD59656.1; -; Genomic_DNA.
DR HSSP; P04578; 1DLB.
DR SMR; Q7ZC00; 83-127, 209-503, 551-637.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Envelope protein; Transmembrane.
SQ SEQUENCE 867 AA; 98421 MW; 7FAA0669D0649A14 CRC64;

Query Match 75.0%; Score 27; DB 2; Length 867;
Best Local Similarity 100.0%; Pred. No. 3.2e-17;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 10 EKSQIQEKNEQELLELDKWSLWNWF 36
Db 658 EKSQIQEKNEQELLELDKWSLWNWF 684

RESULT 9
Q7ZC01_9HIV1 PRELIMINARY; PRT; 868 AA.
AC Q7ZC01;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE Envelope glycoprotein.
GN Name=gp160;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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OC	Lentivirus; Primate lentivirus group.
ON	NCBI_TaxID=11676;
OX	[1]
RP	NCLEOTIDE SEQUENCE.
RX	MEDLINE=94211861; PubMed=7512731;
RA	Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA	Keiler P.M., Shaw A.R., Emini E.A.;
RT	"Neutralization of divergent human immunodeficiency virus type 1
RT	variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT	monoclonal antibody.";
RL	Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR	EMBL; U06723; AAA19138.1; -; mRNA.
DR	HSSP; P31872; 1LB0.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0019031; C:viral envelope; IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR000328; Env_GP41.
DR	Pfam; PF00517; GP41; 1.
FT	NON_TER 1 1
FT	NON_TER 34 34
SEQ	SEQUENCE 34 AA; 4196 MW; OC7CAA60A164B99C CRC64;
Query Match 69.4%; Score 25; DB 2; Length 34;	
Best Local Similarity 100.0%; Pred.No.1.5e-16;	
Matches 25; Conservative 0; Mismatches 0; Indels 0;	
QY	12 SQIQEKNEQELLELDKWASLWNWF 36
DB	10 SQIQEKNEQELLELDKWASLWNWF 34
RESULT 12	
ID	G69895_9HIV1 PRELIMINARY; PRT; 49 AA.
AC	G69895;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Gp41 (Fragment).
GN	Name=env;
OS	Human immunodeficiency virus 1.
OS	Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovir
OC	Lentivirus; Primate lentivirus group.
ON	NCBI_TaxID=11676;
OX	[1]
RP	NCLEOTIDE SEQUENCE.
RX	MEDLINE=94211861; PubMed=7512731;
RA	Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA	Keiler P.M., Shaw A.R., Emini E.A.;
RT	"Neutralization of divergent human immunodeficiency virus type 1
RT	variants and primary isolates by IAM-41-2F5, an anti-gp41 human
RT	monoclonal antibody.";
RL	Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352(1994).
DR	EMBL; U06725; AAA19138.1; -; mRNA.
DR	HSSP; P31872; 1LB0.
DR	GO; GO:0016021; C:integral to membrane; IEA.
DR	GO; GO:0019031; C:viral envelope; IEA.
DR	GO; GO:0005198; F:structural molecule activity; IEA.
DR	InterPro; IPR000328; Env_GP41.
DR	Pfam; PF00517; GP41; 1.
FT	NON_TER 1 1
FT	NON_TER 49 49
SEQ	SEQUENCE 49 AA; 6168 MW; 8077C4815B83281E CRC64;
Query Match 69.4%; Score 25; DB 2; Length 49;	
Best Local Similarity 100.0%; Pred.No.2e-16;	
Matches 25; Conservative 0; Mismatches 0; Indels 0;	
QY	12 SQIQEKNEQELLELDKWASLWNWF 36
DB	25 SQIQEKNEQELLELDKWASLWNWF 49



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RESULT 13
Q69896 9HIV1
ID Q69896 9HIV1 PRELIMINARY; PRT; 49 AA.
AC Q69896;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp41 (Fragment).
EN
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94211861; PubMed=7512731;
RA Conley A.J., Kessler J.A., Boots L.J., Tung J.S., Arnold B.A.,
RA Keller P.M., Shaw A.R., Emini E.A.;
RT "Neutralization of divergent human immunodeficiency virus type 1
RT variants and primary isolates by IAM-41-2FS, an anti-gp41 human
RT monoclonal antibody."
RL Proc. Natl. Acad. Sci. U.S.A. 91:3348-3352 (1994).
DR EMBL; U06726; AAA19139.1; -; mRNA.
DR HSSP; P31872; 1LB0.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 6167 MW; 0277C4815B8D26FE CRC64;

Query Match 69.4%; Score 25; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQQEKNEQELLELDKWSLWNWF 36
Db 25 SQIQQEKNEQELLELDKWSLWNWF 49

RESULT 14
Q9ES53 9HIV1
ID Q9ES53 9HIV1 PRELIMINARY; PRT; 118 AA.
AC Q9ES53;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
EN
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=CAM11;
RX MEDLINE=20414627; PubMed=10957729; DOI=10.1089/08892220050117087;
RA Peter F.N., Bittel M.N., Judith T.N., George A.A., Laura E.T.,
RA John N.N., Feng G., Mark R., Thomas F.M., Danuta P., Renu L.B.;
RT "Presence of Diverse Human Immunodeficiency Virus Type 1 Viral
RT Variants in Cameroon."
RL AIDS Res. Hum. Retroviruses 16:1319-1324 (2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=CAM11;
RA Fonjongo P.N., Mpoudi E.N., Torimiro J.N., Alemnji G.A., Eno L.T.,
RA Ngngasong J.N., Gao F., Rayfield M., Folks T.M., Pieniazek D.,
RA Lal R.B.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF252098; AAG14307.1; -; Genomic DNA.
DR HSSP; P31872; 1LB0.
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DR SMR; Q9ES53; 1-101.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 14275 MW; 1878D17C292899C0 CRC64;

Query Match 69.4%; Score 25; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 4.5e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQQEKNEQELLELDKWSLWNWF 36
Db 85 SQIQQEKNEQELLELDKWSLWNWF 109

RESULT 15
Q6WH14 9HIV1
ID Q6WH14 9HIV1 PRELIMINARY; PRT; 121 AA.
AC Q6WH14;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein (Fragment).
EN
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14715797; DOI=10.1128/JCM.42.1.426-430.2004;
RA Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,
RA Gouvea M.I.F.S., Guimaraes M.A.A.M., De Oliveira F.E.,
RA Magnanini M.M.F., Brindeiro R.M., Tanuri A.;
RT "Prevalence of human immunodeficiency virus drug resistance mutations
RT and subtypes in drug-naive, infected individuals in the army health
RT service of Rio de Janeiro, Brazil."
RL J. Clin. Microbiol. 42:426-430 (2004).
DR EMBL; AY285082; AAQ68145.1; -; Genomic RNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000328; Env_GP41.
DR Pfam; PF00517; GP41; 1.
KW Envelope protein.
FT NON_TER 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 14619 MW; E2791CC4069F12F8 CRC64;

Query Match 69.4%; Score 25; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 4.6e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQQEKNEQELLELDKWSLWNWF 36
Db 88 SQIQQEKNEQELLELDKWSLWNWF 112

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Job time : 122 secs
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 6, 2006, 16:25:38 ; Search time 28.6667 Seconds  
(without alignments)  
103.825 Million cell updates/sec

Title: US-09-809-060A-4  
Perfect score: 36  
Sequence: 1 YTSLLVLSKSIQKNEQELLEDKWSLWNP 36

Scoring table: OIIGO

Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size : 0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgn2\_6/ptodata/1/iaa/6 COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/H COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/RE COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	100.0	36	2	US-08-484-223B-240
2	36	100.0	36	2	US-09-082-279B-1360
3	36	100.0	36	2	US-09-315-304B-1360
4	36	100.0	36	2	US-09-834-784-1360
5	36	100.0	36	2	US-09-515-965A-1360
6	36	100.0	36	2	US-09-350-641C-1360
7	36	100.0	36	2	US-09-350-841A-1360
8	25	69.4	36	2	US-09-515-965A-1986
9	25	69.4	36	2	US-09-350-641C-1749
10	25	69.4	36	2	US-09-350-841A-1938
11	25	69.4	138	2	US-09-570-921-10
12	25	69.4	268	2	US-08-965-056-7
13	25	69.4	269	2	US-08-965-056-21
14	24	66.7	36	2	US-09-082-279B-1361
15	24	66.7	36	2	US-09-315-304B-1361
16	24	66.7	36	2	US-09-834-784-1361
17	24	66.7	36	2	US-09-515-965A-1361
18	24	66.7	36	2	US-09-350-641C-1361
19	24	66.7	36	2	US-09-350-841A-1361
20	22	61.1	22	1	US-08-073-028-61
21	22	61.1	22	2	US-08-554-616-61
22	22	61.1	22	2	US-09-515-965A-1674
23	22	61.1	22	2	US-09-350-841A-1704
24	22	61.1	22	2	US-10-005-305-53
25	22	61.1	22	2	US-10-005-305-78
26	22	61.1	23	1	US-08-073-028-62
27	22	61.1	23	2	US-08-484-223B-237

Query Match 100.0%; Score 36; DB 2; Length 36;

28 22 61.1 23 2 US-08-554-616-62 Sequence 62, Appl  
29 22 61.1 23 2 US-09-082-279B-59 Sequence 59, Appl  
30 22 61.1 23 2 US-08-474-349A-421 Sequence 421, Appl  
31 22 61.1 23 2 US-09-315-304B-59 Sequence 59, Appl  
32 22 61.1 23 2 US-09-834-784-59 Sequence 59, Appl  
33 22 61.1 23 2 US-09-515-965A-59 Sequence 1675, Ap  
34 22 61.1 23 2 US-09-350-641C-59 Sequence 59, Appl  
35 22 61.1 23 2 US-09-350-841A-59 Sequence 59, Appl  
36 22 61.1 23 2 US-09-350-841A-1705 Sequence 1705, Ap  
37 22 61.1 23 2 US-08-487-266A-237 Sequence 237, Ap  
38 22 61.1 23 2 US-10-005-305-54 Sequence 54, Appl  
39 22 61.1 23 2 US-10-005-305-77 Sequence 77, Appl  
40 22 61.1 23 2 US-08-073-028-63 Sequence 63, Appl  
41 22 61.1 24 1 US-08-554-616-63 Sequence 63, Appl  
42 22 61.1 24 2 US-09-082-279B-789 Sequence 789, App  
43 22 61.1 24 2 US-09-082-279B-790 Sequence 790, App  
44 22 61.1 24 2 US-09-315-304B-789 Sequence 789, App  
45 22 61.1 24 2

#### ALIGNMENTS

RESULT 1  
US-08-484-223B-240  
; Sequence 240, Application US/08484223B  
; Patent No. 6020459  
; GENERAL INFORMATION:  
; APPLICANT: Bolognesi, Dani P.  
; APPLICANT: Matthews, Thomas J.  
; APPLICANT: Wild, Carl T.  
; APPLICANT: Barney, Shawn O.  
; APPLICANT: Lambert, Dennis M.  
; APPLICANT: Petteway, Stephen R.  
; APPLICANT: Langlois, Alphonse J.  
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF  
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV  
; NUMBER OF SEQUENCES: 245  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/484,223B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7872-029  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-9741/8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 240:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 36 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
US-08-484-223B-240

Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLEKSIQOEKNEQELLELDKWASLWNWF 36  
Db 1 YTSLIYSLEKSIQOEKNEQELLELDKWASLWNWF 36

## RESULT 2

US-09-082-279B-1360  
; Sequence 1360, Application US/09082279B  
; Patent No. 6258782  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/082,279B  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1360  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-082-279B-1360

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLEKSIQOEKNEQELLELDKWASLWNWF 36  
Db 1 YTSLIYSLEKSIQOEKNEQELLELDKWASLWNWF 36

## RESULT 3

US-09-315-304B-1360  
; Sequence 1360, Application US/09315304B  
; Patent No. 6348568  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; FILE REFERENCE: 7872-052  
; CURRENT APPLICATION NUMBER: US/09/315,304B  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1667  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1360  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-315-304B-1360

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Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLEKSIQOEKNEQELLELDKWASLWNWF 36  
Db 1 YTSLIYSLEKSIQOEKNEQELLELDKWASLWNWF 36

## RESULT 4

US-09-834-784-1360  
; Sequence 1360, Application US/09834784  
; Patent No. 6562787  
; GENERAL INFORMATION:  
; APPLICANT: Barney, Shawn  
; APPLICANT: Guthrie, Kelly  
; APPLICANT: Merutka, Gene  
; APPLICANT: Anwer, Mohamed  
; APPLICANT: Lambert, Dennis  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED  
; FILE REFERENCE: 7872-043  
; CURRENT APPLICATION NUMBER: US/09/834,784  
; PRIOR FILING DATE: 2001-04-13  
; CURRENT APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1515  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1360  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-834-784-1360

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLEKSIQOEKNEQELLELDKWASLWNWF 36  
Db 1 YTSLIYSLEKSIQOEKNEQELLELDKWASLWNWF 36

## RESULT 5

US-09-515-965A-1360  
; Sequence 1360, Application US/09515965A  
; Patent No. 6623741  
; GENERAL INFORMATION:  
; APPLICANT: Antczak, J.  
; APPLICANT: Delmedico, M.  
; APPLICANT: Erickson, J.  
; APPLICANT: Lambert, D.  
; APPLICANT: Sista, P.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-  
; FILE REFERENCE: 7872-073  
; CURRENT APPLICATION NUMBER: US/09/515,965A  
; PRIOR FILING DATE: 2000-02-29  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1994  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1360  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-09-515-965A-1360

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36  
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## RESULT 6

US-09-350-641C-1360

; Sequence 1360, Application US/09350641C

; Patent No. 6656906

; GENERAL INFORMATION:

; APPLICANT: Barney, S.

; APPLICANT: Guthrie, K.

; APPLICANT: Merutka, G.

; APPLICANT: Anwer, M.

; APPLICANT: Lambert, D.

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

; FILE REFERENCE: 7872-067

; CURRENT APPLICATION NUMBER: US/09/350.641C

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: 09/315,304

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/082,279

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1757

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-350-641C-1360

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36  
Db 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36

## RESULT 7

US-09-350-841A-1360

; Sequence 1360, Application US/09350841A

; Patent No. 6750008

; GENERAL INFORMATION:

; APPLICANT: Jeffes, Peter;

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE

; FILE REFERENCE: 7872-066-999

; CURRENT APPLICATION NUMBER: US/09/350.841A

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 1946

; SOFTWARE: Patent In Ver. 2.1

; SEQ ID NO 1360

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-350-841A-1360

Query Match 100.0%; Score 36; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-26;  
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36  
Db 1 YTSLSLLEKSIQIQEKNEQELLELDKQWASLWNWF 36

## RESULT 8

US-09-515-965A-1986

; Sequence 1986, Application US/09515965A

; Patent No. 6623741

; GENERAL INFORMATION:

; APPLICANT: Antczak, J.

; APPLICANT: Delmedico, M.

; APPLICANT: Erickson, J.

; APPLICANT: Lambert, D.

; APPLICANT: Sista, P.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-

; FILE REFERENCE: 7872-073

; CURRENT APPLICATION NUMBER: US/09/515.965A

; PRIOR FILING DATE: 2000-02-29

; PRIOR APPLICATION NUMBER: 09/315,304

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/082,279

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1994

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1986

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-515-965A-1986

Query Match 69.4%; Score 25; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3e-16;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKQWASLWNWF 36  
Db 12 SQIQEKNEQELLELDKQWASLWNWF 36

## RESULT 9

US-09-350-641C-1749

; Sequence 1749, Application US/09350641C

; Patent No. 6656906

; GENERAL INFORMATION:

; APPLICANT: Barney, S.

; APPLICANT: Guthrie, K.

; APPLICANT: Merutka, G.

; APPLICANT: Anwer, M.

; APPLICANT: Lambert, D.

; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC

; FILE REFERENCE: 7872-067

; CURRENT APPLICATION NUMBER: US/09/350.641C

; PRIOR FILING DATE: 1999-07-09

; PRIOR APPLICATION NUMBER: 09/315,304

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: 09/082,279

; PRIOR FILING DATE: 1998-05-20

; NUMBER OF SEQ ID NOS: 1757

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 1749

; LENGTH: 36

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Core polypeptide

US-09-350-641C-1749

Query Match 69.4%; Score 25; DB 2; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3e-16;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKQWASLWNWF 36

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Db 12 SQIQEKNEQELLELDKWSLWNWF 36
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RESULT 10
US-09-350-841A-1938
; Sequence 1938, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffes, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350.841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1938
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-09-350-841A-1938
Query Match 69.4%; Score 25; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
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Db 12 SQIQEKNEQELLELDKWSLWNWF 36
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RESULT 11
US-09-570-921-10
; Sequence 10, Application US/09570921
; Patent No. 6455265
; GENERAL INFORMATION:
; APPLICANT: SERRES, PIERRE-FRANCOIS
; TITLE OF INVENTION: METHOD FOR OBTAINING VACCINES FOR PREVENTING THE
; FILE REFERENCE: 106213
; CURRENT APPLICATION NUMBER: US/09/570.921
; CURRENT FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: PCT/FR98/02447
; PRIOR FILING DATE: 1998-11-17
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Human
US-09-570-921-10
Query Match 69.4%; Score 25; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 9.9e-16;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
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Db 110 SQIQEKNEQELLELDKWSLWNWF 134
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RESULT 12
US-08-965-056-7
; Sequence 7, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
```

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; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 268 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: HIV-JRCSP
US-08-965-056-7
Query Match 69.4%; Score 25; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQIQEKNEQELLELDKWSLWNWF 36
|||||
Db 179 SQIQEKNEQELLELDKWSLWNWF 203
|||||

RESULT 13
US-08-965-056-21
; Sequence 21, Application US/08965056
; Patent No. 6271198
; GENERAL INFORMATION:
; APPLICANT: Andrew C. Braisted
; APPLICANT: J. Kevin Judice
; APPLICANT: Robert S. McDowell
; APPLICANT: J. Christopher Phelan
; APPLICANT: Melissa A. Starovasnik
; APPLICANT: James A. Wells
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,056
; FILING DATE: 05-No. 6271198-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1005R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 269 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-965-056-21

Query Match 69.4%; Score 25; DB 2; Length 269;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 SQQQKNEQELLELDKWSLWVNF 36
Db 180 SQQQKNEQELLELDKWSLWVNF 204

RESULT 14
US-09-082-279B-1361
; Sequence 1361, Application US/09082279B
; Patent No. 6258782
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn
; APPLICANT: Guthrie, Kelly
; APPLICANT: Merutka, Gene
; APPLICANT: Anwer, Mohamed
; APPLICANT: Lambert, Dennis
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES
; FILE REFERENCE: 7872-043
; CURRENT APPLICATION NUMBER: US/09/082,279B
; CURRENT FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1515
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1361
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-082-279B-1361

Query Match 66.7%; Score 24; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQLQEKNEQELL 24
Db 1 YTSLIYSLLEKSQLQEKNEQELL 24

RESULT 15
US-09-315-304B-1361
; Sequence 1361, Application US/09315304B
; Patent No. 6348568
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
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; FILE REFERENCE: 7872-052
; CURRENT APPLICATION NUMBER: US/09/315,304B
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1667
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1361
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
; US-09-315-304B-1361

Query Match 66.7%; Score 24; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.4e-15;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQLQEKNEQELL 24
Db 1 YTSLIYSLLEKSQLQEKNEQELL 24

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

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(without alignments)  
154.540 Million cell updates/sec

Title: US-09-809-060A-4  
Perfect score: 36  
Sequence: 1 YTSLYSLEKSQIQEQNEQELLELDKWSLWNWF 36

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	36	100.0	36	3	US-09-809-060-4	Sequence 4, Appli
2	36	100.0	36	4	US-10-351-641-1360	Sequence 1360, Ap
3	36	100.0	36	4	US-10-663-583-40	Sequence 40, Appl
4	36	100.0	36	4	US-10-671-282-40	Sequence 40, Appl
5	36	100.0	36	5	US-10-168-295-5	Sequence 5, Appli
6	36	100.0	36	5	US-10-168-295-57	Sequence 57, Appl
7	25	69.4	36	4	US-10-351-641-1749	Sequence 1749, Ap
8	25	69.4	268	3	US-09-854-816-7	Sequence 7, Appli
9	25	69.4	269	3	US-09-854-816-21	Sequence 21, Appl
10	24	66.7	36	4	US-10-351-641-1361	Sequence 1361, Ap
11	22	61.1	22	4	US-10-005-305-53	Sequence 53, Appl
12	22	61.1	22	4	US-10-005-305-78	Sequence 78, Appl
13	22	61.1	22	5	US-10-950-010-130	Sequence 130, App
14	22	61.1	23	4	US-10-351-641-59	Sequence 59, Appl
15	22	61.1	23	4	US-10-005-305-54	Sequence 54, Appl
16	22	61.1	23	4	US-10-005-305-77	Sequence 77, Appl
17	22	61.1	23	4	US-10-267-682-237	Sequence 237, App
18	22	61.1	23	4	US-10-267-748-237	Sequence 237, App
19	22	61.1	23	5	US-10-168-295-54	Sequence 54, Appl
20	22	61.1	23	5	US-10-950-010-129	Sequence 129, App
21	22	61.1	24	4	US-10-351-641-789	Sequence 789, App
22	22	61.1	24	4	US-10-351-641-790	Sequence 790, App
23	22	61.1	24	4	US-10-005-305-55	Sequence 55, Appl
24	22	61.1	24	4	US-10-005-305-76	Sequence 76, Appl
25	22	61.1	24	4	US-10-005-305-201	Sequence 201, App
26	22	61.1	24	4	US-10-677-807-236	Sequence 236, App
27	22	61.1	24	5	US-10-950-010-128	Sequence 128, App

## ALIGNMENTS

## RESULT 1

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US-09-809-060-4
; Sequence 4, Application US/09809060
; Publication No. US20020010317A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Carl T.
; APPLICANT: Allaway, Graham P.
; TITLE OF INVENTION: A Method for Genotyping
; TITLE OF INVENTION: Neutralizing Antibodies
; TITLE OF INVENTION: Regions of HIV-1
; FILE REFERENCE: 1900.0260001
; CURRENT APPLICATION NUMBER: US/09/09809060
; CURRENT FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 60/188000
; PRIOR FILING DATE: 2000-03-17
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-809-060-4

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Query Match      100.0%; Score 36; DB 3; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YTSLSYLLLEKSIQIQOEKNEQELLELDKQWASLWNWF 36
    |||||
Db 1 YTSLSYLLLEKSIQIQOEKNEQELLELDKQWASLWNWF 36
    |||||

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## RESULT 2

US-001-351-641-1360  
 ; Sequence 1360, Application US/10351641  
 ; Publication No. US20030186874A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Barney, S.  
 ; APPLICANT: Guthrie, K.  
 ; APPLICANT: Merutka, G.  
 ; APPLICANT: Anwer, M.  
 ; APPLICANT: Lambert, D.  
 ; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
 ; TITLE OF INVENTION: PROPERTIES  
 ; FILE REFERENCE: 7872-100  
 ; CURRENT APPLICATION NUMBER: US/10/351,641  
 ; CURRENT FILING DATE: 2003-01-24  
 ; PRIOR APPLICATION NUMBER: 09/350,641  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: 09/315,304

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; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1360
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-1360

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36

RESULT 3
US-10-663-589-40
; Sequence 40, Application US/10663589
; Publication No. US2004006367A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Pharmaceutical composition for improved administration of HIV
; FILE REFERENCE: TRM-003
; CURRENT APPLICATION NUMBER: US/10/663,589
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 60/414,441
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthesized
US-10-663-589-40

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36

RESULT 4
US-10-671-282-40
; Sequence 40, Application US/10671282
; Publication No. US20040122214A1
; GENERAL INFORMATION:
; APPLICANT: Trimeris, Inc.
; TITLE OF INVENTION: Conjugates comprised of polymer and HIV gp41-derived peptides and
; FILE REFERENCE: TRM-004
; CURRENT APPLICATION NUMBER: US/10/671,282
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: 60/414,439
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial
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; FEATURE:
; OTHER INFORMATION: synthesized
US-10-671-282-40

Query Match      100.0%; Score 36; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36

RESULT 5
US-10-168-295-5
; Sequence 5, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Baroudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-5

Query Match      100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36

RESULT 6
US-10-168-295-57
; Sequence 57, Application US/10168295
; Publication No. US20050065319A1
; GENERAL INFORMATION:
; APPLICANT: Baroudy, Bahige M.
; TITLE OF INVENTION: Combination Method For Treating Viral Infections
; FILE REFERENCE: IN01358
; CURRENT APPLICATION NUMBER: US/10/168,295
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: PCT/US01/48802
; PRIOR FILING DATE: 2000-12-17
; PRIOR APPLICATION NUMBER: 60/256,657
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-168-295-57

Query Match      100.0%; Score 36; DB 5; Length 36;
Best Local Similarity 100.0%; Pred. No. 2.1e-26;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
   |||||
Db 1 YTSLIYSLLEKSQIQEKNEQELLELDKWASLWNWF 36
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RESULT 7  
US-10-351-641-1749  
; Sequence 1749, Application US/10351641  
; Publication No. US20030186674A1  
; GENERAL INFORMATION:  
; APPLICANT: Barney, S.  
; APPLICANT: Guthrie, K.  
; APPLICANT: Merutka, G.  
; APPLICANT: Anwer, M.  
; APPLICANT: Lambert, D.  
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC  
; TITLE OF INVENTION: PROPERTIES  
; FILE REFERENCE: 7872-100  
; CURRENT APPLICATION NUMBER: US/10/351,641  
; CURRENT FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: 09/350,641  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 09/315,304  
; PRIOR FILING DATE: 1999-05-20  
; PRIOR APPLICATION NUMBER: 09/082,279  
; PRIOR FILING DATE: 1998-05-20  
; NUMBER OF SEQ ID NOS: 1757  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1749  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Core polypeptide  
US-10-351-641-1749  
  
Query Match 69.4%; Score 25; DB 4; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.8e-16; Indels 0; Gaps 0;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 12 SQIQEKNEQELLELDKWASLWNWF 36  
Db 12 SQIQEKNEQELLELDKWASLWNWF 36  
  
RESULT 8  
US-09-854-816-7  
; Sequence 7, Application US/09854816  
; Patent No. US20020151473A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew C. Braisted  
; J. Kevin Judice  
; Robert S. McDowell  
; J. Christopher Phelan  
; Melissa A. Starovasnik  
; James A. Wells  
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
; Making Same  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/854,816  
; FILING DATE: 15-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/965,056  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, PhD., Timothy E.  
; REGISTRATION NUMBER: 36,700  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 269 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:

; APPLICATION NUMBER: 08/965,056  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, PhD., Timothy E.  
; REGISTRATION NUMBER: 36,700  
; REFERENCE/DOCKET NUMBER: P1005R2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 269 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; MOLECULE TYPE: HIV-JRC5F  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-09-854-816-7  
  
Query Match 69.4%; Score 25; DB 3; Length 268;  
Best Local Similarity 100.0%; Pred. No. 2.2e-15;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 12 SQIQEKNEQELLELDKWASLWNWF 36  
Db 179 SQIQEKNEQELLELDKWASLWNWF 203  
  
RESULT 9  
US-09-854-816-21  
; Sequence 21, Application US/09854816  
; Patent No. US20020151473A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew C. Braisted  
; J. Kevin Judice  
; Robert S. McDowell  
; J. Christopher Phelan  
; Melissa A. Starovasnik  
; James A. Wells  
; TITLE OF INVENTION: Constrained Helical Peptides and Methods of  
; Making Same  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/854,816  
; FILING DATE: 15-May-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/965,056  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Torchia, PhD., Timothy E.  
; REGISTRATION NUMBER: 36,700  
; TELEPHONE: 650/225-8674  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 269 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:



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; NUMBER OF SEQ ID NOS: 545
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 130
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-950-010-130

Query Match      61.1%; Score 22; DB 5; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKQWASLWNWF 36
Db 1 QOEKNEQELLELDKQWASLWNWF 22

RESULT 14
US-10-351-641-59
; Sequence 59, Application US/10351641
; Publication No. US20030186874A1
; GENERAL INFORMATION:
; APPLICANT: Barney, S.
; APPLICANT: Guthrie, K.
; APPLICANT: Merutka, G.
; APPLICANT: Anwer, M.
; APPLICANT: Lambert, D.
; TITLE OF INVENTION: HYBRID POLYPEPTIDES WITH ENHANCED PHARMACOKINETIC
; TITLE OF INVENTION: PROPERTIES
; FILE REFERENCE: 7872-100
; CURRENT APPLICATION NUMBER: US/10/351,641
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: 09/350,641
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 09/315,304
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: 09/082,279
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 1757
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Core polypeptide
US-10-351-641-59

Query Match      61.1%; Score 22; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKQWASLWNWF 36
Db 2 QOEKNEQELLELDKQWASLWNWF 23

RESULT 15
US-10-005-305-54
; Sequence 54, Application US/10005305
; Publication No. US20030203841A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, represented by the
; APPLICANT: Secretary, Department of Health and Human Services
; TITLE OF INVENTION: T20/DP178 AND T21/DP107 ARE ACTIVATORS
; TITLE OF INVENTION: OF HUMAN PHAGOCYTE
; TITLE OF INVENTION: FORMYL PEPTIDE RECEPTORS
; FILE REFERENCE: NIH171.001C1
; CURRENT APPLICATION NUMBER: US/10/005,305
; CURRENT FILING DATE: 2001-11-02
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; PRIOR APPLICATION NUMBER: PCT/US00/12371
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,686
; PRIOR FILING DATE: 1999-05-05
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-005-305-54

Query Match      61.1%; Score 22; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKQWASLWNWF 36
Db 2 QOEKNEQELLELDKQWASLWNWF 23

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GenCore version 5.1.7

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OM protein - protein search, using sw model

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Title: US-09-809-060A-4

Perfect score: 36

Sequence: 1 YTSIYSLLEKSIQOEKNEQELLELDKWSLWNWF 36

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OLIGO Gapop 60.0 , Gapext 60.0

Searched: 135346 seqs, 20000420 residues

Word size : 0

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

Database : Published Applications AA.New.\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*
- 5: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*
- 7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	61.1	35	6	US-10-506-796A-1
2	22	61.1	36	6	US-10-841-956A-1
3	22	61.1	36	6	US-10-506-796A-3
4	22	61.1	36	7	US-11-029-003-1
5	22	61.1	36	7	US-11-187-687-22
6	22	61.1	37	7	US-11-112-277-33
7	22	61.1	44	7	US-11-089-426-10
8	22	61.1	44	7	US-11-187-687-24
9	22	61.1	145	7	US-11-084-858-11
10	22	61.1	171	6	US-10-506-796A-9
11	22	61.1	267	6	US-10-841-956A-4
12	22	61.1	269	6	US-10-841-956A-8
13	22	61.1	270	6	US-10-841-956A-5
14	22	61.1	281	6	US-10-841-956A-7
15	22	61.1	282	6	US-10-841-956A-6
16	22	61.1	293	6	US-10-841-956A-9
17	22	61.1	354	7	US-11-053-100-27
18	22	61.1	356	7	US-11-053-100-36
19	22	61.1	357	7	US-11-053-100-30
20	22	61.1	357	7	US-11-053-100-33
21	22	61.1	504	7	US-11-053-100-28
22	22	61.1	506	7	US-11-053-100-37
23	22	61.1	507	7	US-11-053-100-31
24	22	61.1	507	7	US-11-053-100-34
25	22	61.1	654	7	US-11-053-100-29

26	22	61.1	656	7	US-11-053-100-38	Sequence 38, Appl
27	22	61.1	657	7	US-11-053-100-32	Sequence 32, Appl
28	22	61.1	657	7	US-11-053-100-35	Sequence 35, Appl
29	22	61.1	856	6	US-10-510-947-8	Sequence 8, Appl
30	22	61.1	856	7	US-11-042-988-13	Sequence 13, Appl
31	22	61.1	856	7	US-11-135-235-1	Sequence 1, Appl
32	16	44.4	36	6	US-10-506-796A-5	Sequence 5, Appl
33	15	41.7	15	7	US-11-045-024-13381	Sequence 13381, A
34	15	41.7	601	7	US-11-014-842A-37	Sequence 37, Appl
35	15	41.7	613	7	US-11-014-842A-33	Sequence 33, Appl
36	15	41.7	669	7	US-11-014-842A-29	Sequence 29, Appl
37	15	41.7	681	7	US-11-014-842A-25	Sequence 25, Appl
38	15	41.7	789	7	US-11-014-842A-39	Sequence 39, Appl
39	15	41.7	801	7	US-11-014-842A-35	Sequence 35, Appl
40	15	41.7	857	7	US-11-014-842A-31	Sequence 31, Appl
41	15	41.7	869	7	US-11-014-842A-27	Sequence 27, Appl
42	14	38.9	36	6	US-10-506-796A-7	Sequence 7, Appl
43	11	30.6	11	7	US-11-045-024-101	Sequence 101, App
44	11	30.6	11	7	US-11-045-024-103	Sequence 103, App
45	11	30.6	11	7	US-11-045-024-983	Sequence 983, App

## ALIGNMENTS

RESULT 1  
 US-10-506-796A-1  
 ; Sequence 1, Application US/10506796A  
 ; Publication No. US200600113831A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MOR, Tsafir  
 ; APPLICANT: MATOBA, Nobuyuki  
 ; APPLICANT: ARNTZEN, Charles  
 ; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE  
 ; FILE REFERENCE: 01231.0006U2  
 ; CURRENT APPLICATION NUMBER: US/10/506,796A  
 ; PRIOR FILING DATE: 2004-09-03  
 ; PRIOR APPLICATION NUMBER: PCT/US03/07073  
 ; PRIOR FILING DATE: 2003-03-06  
 ; PRIOR APPLICATION NUMBER: 60/362,247  
 ; PRIOR FILING DATE: 2002-03-06  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 1  
 ; TYPE: PRT  
 ; ORGANISM: Human immunodeficiency virus type 1  
 ; FEATURE:  
 ; NAME/KEY: PEPTIDE  
 ; LOCATION: (1)..(35)  
 ; OTHER INFORMATION: HIV-1 gp41 peptide portion (residues 650-685)  
 US-10-506-796A-1

Query Match 61.1%; Score 22; DB 6; Length 35;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-15;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKWSLWNWF 36  
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 Db 4 QOEKNEQELLELDKWSLWNWF 25

RESULT 2  
 US-10-841-956A-1  
 ; Sequence 1, Application US/10841956A  
 ; Publication No. US20050281829A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TAN HEHIR, CRISTINA A.  
 ; APPLICANT: MEZO, ADAM R.  
 ; APPLICANT: PETERS, ROBERT T.  
 ; APPLICANT: STATTEL, JAMES M.  
 ; APPLICANT: PALOMBELLA, VITO J.  
 ; APPLICANT: BITONTI, ALAN R.

; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS  
; FILE REFERENCE: 08945.0003-00000  
; CURRENT APPLICATION NUMBER: US/10/841,956A  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: 60/468,835  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-10-841-956A-1

Query Match 61.1%; Score 22; DB 6; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-15; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 15 QOEKNEQELLELDKWASLWNWF 36  
Db 15 QOEKNEQELLELDKWASLWNWF 36

RESULT 3  
US-10-506-796A-3  
; Sequence 3, Application US/10506796A  
; Publication No. US20060013831A1  
; GENERAL INFORMATION:  
; APPLICANT: MOR, Tsafir  
; APPLICANT: MATOBA, Nobuyuki  
; APPLICANT: ARNTZEN, Charles  
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE  
; FILE REFERENCE: 01231.0006U2  
; CURRENT APPLICATION NUMBER: US/10/506,796A  
; CURRENT FILING DATE: 2004-09-03  
; PRIOR APPLICATION NUMBER: PCT/US03/07073  
; PRIOR FILING DATE: 2003-03-06  
; PRIOR APPLICATION NUMBER: 60/362,247  
; PRIOR FILING DATE: 2002-03-06  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus type 1  
US-10-506-796A-3

Query Match 61.1%; Score 22; DB 6; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-15; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 15 QOEKNEQELLELDKWASLWNWF 36  
Db 5 QOEKNEQELLELDKWASLWNWF 26

RESULT 4  
US-11-029-003-1  
; Sequence 1, Application US/11029003  
; Publication No. US20050260194A1  
; GENERAL INFORMATION:  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: RIVERA, DANIEL S.  
; APPLICANT: BITONTI, ALAN J.  
; APPLICANT: STATTEL, JAMES  
; TITLE OF INVENTION: IMMUNOGLOBULIN CHIMERIC MONOMER-DIMER HYBRIDS  
; FILE REFERENCE: 08945.0007-01000  
; CURRENT APPLICATION NUMBER: US/11/029,003  
; CURRENT FILING DATE: 2005-01-05  
; PRIOR APPLICATION NUMBER: 60/539,207  
; PRIOR FILING DATE: 2004-01-26  
; PRIOR APPLICATION NUMBER: 60/487,964

; PRIOR FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: 60/469,600  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 1  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-11-029-003-1

Query Match 61.1%; Score 22; DB 7; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-15; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 15 QOEKNEQELLELDKWASLWNWF 36  
Db 15 QOEKNEQELLELDKWASLWNWF 36

RESULT 5  
US-11-187-687-22  
; Sequence 22, Application US/11187687  
; Publication No. US20060019347A1  
; GENERAL INFORMATION:  
; APPLICANT: Cho, Ho Sung  
; APPLICANT: Daniel, Thomas O.  
; APPLICANT: Hays, Anna-Maria  
; APPLICANT: Wilson, Troy E.  
; APPLICANT: Litzinger, David C.  
; APPLICANT: Mariani, Roberto  
; APPLICANT: Kimmel, Bruce E.  
; APPLICANT: Keefe, William M.  
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino  
; FILE REFERENCE: AMBX-0041.000US  
; CURRENT APPLICATION NUMBER: US/11/187,687  
; CURRENT FILING DATE: 2005-07-21  
; PRIOR APPLICATION NUMBER: 60/590,035  
; PRIOR FILING DATE: 2004-07-21  
; PRIOR APPLICATION NUMBER: 60/659,709  
; PRIOR FILING DATE: 2005-03-07  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 22  
; LENGTH: 36  
; TYPE: PRT  
; ORGANISM: Human immunodeficiency virus  
US-11-187-687-22

Query Match 61.1%; Score 22; DB 7; Length 36;  
Best Local Similarity 100.0%; Pred. No. 2.8e-15; Indels 0; Gaps 0;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 15 QOEKNEQELLELDKWASLWNWF 36  
Db 15 QOEKNEQELLELDKWASLWNWF 36

RESULT 6  
US-11-112-277-33  
; Sequence 33, Application US/11112277  
; Publication No. US20050267293A1  
; GENERAL INFORMATION:  
; APPLICANT: Bousquet-Gagnon, Nathalie  
; APPLICANT: Quraishi, Omar  
; APPLICANT: Bridon, Dominique P.  
; TITLE OF INVENTION: METHOD FOR THE PURIFICATION OF ALBUMIN  
; FILE REFERENCE: 500862003700  
; CURRENT APPLICATION NUMBER: US/11/112,277  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/565,238



; PRIOR FILING DATE: 2004-04-23  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 33  
; LENGTH: 37  
; TYPE: PR1  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: T20 Analogue  
; FEATURE:  
; NAME/KEY: MOD\_RES  
; LOCATION: 37  
; OTHER INFORMATION: Xaa is Lys linked to AEEA-MPA  
US-11-112-277-33

Query Match 61.1%; Score 22; DB 7; Length 37;  
Best Local Similarity 100.0%; Pred. No. 2.9e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKQASLWVWF 36  
Db 15 QOEKNEQELLELDKQASLWVWF 36

## RESULT 7

US-11-089-426-10  
; Sequence 10, Application US/11089426  
; Publication No. US20050261229A1  
; GENERAL INFORMATION:  
; APPLICANT: Lo, Kin-Ming  
; APPLICANT: Wesolowski, John  
; TITLE OF INVENTION: FC Fusion Proteins For Enhancing the Immunogenicity of  
; TITLE OF INVENTION: Protein and Peptide Antigens  
; FILE REFERENCE: LEX-007  
; CURRENT APPLICATION NUMBER: US/11/089,426  
; CURRENT FILING DATE: 2005-03-24  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: US/09/621,268  
; PRIOR FILING DATE: 2000-07-21  
; PRIOR APPLICATION NUMBER: US 60/144,965  
; PRIOR FILING DATE: 1999-07-21  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 44  
; TYPE: PR1  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:Fused  
; OTHER INFORMATION: polypeptide from pDC-muFC vector  
US-11-089-426-10

Query Match 61.1%; Score 22; DB 7; Length 44;  
Best Local Similarity 100.0%; Pred. No. 3.4e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKQASLWVWF 36  
Db 13 QOEKNEQELLELDKQASLWVWF 34

## RESULT 8

US-11-187-687-24  
; Sequence 24, Application US/11187687  
; Publication No. US20060019347A1  
; GENERAL INFORMATION:  
; APPLICANT: Cho, Ho Sung.  
; APPLICANT: Daniel, Thomas O.  
; APPLICANT: Hays, Anna-Maria  
; APPLICANT: Wilson, Troy E.  
; APPLICANT: Litzinger, David C.  
; APPLICANT: Mariani, Roberto  
; APPLICANT: Kimmel, Bruce E.

; APPLICANT: Keefe, William M.  
; TITLE OF INVENTION: Biosynthetic Polypeptides Utilizing Non-Naturally Encoded Amino  
; FILE REFERENCE: AMBX-0041.00US  
; CURRENT APPLICATION NUMBER: US/11/187,687  
; CURRENT FILING DATE: 2005-07-21  
; PRIOR APPLICATION NUMBER: 60/590,035  
; PRIOR FILING DATE: 2004-07-21  
; PRIOR APPLICATION NUMBER: 60/659,709  
; PRIOR FILING DATE: 2005-03-07  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 24  
; LENGTH: 44  
; TYPE: PR1  
; ORGANISM: Human immunodeficiency virus  
US-11-187-687-24

Query Match 61.1%; Score 22; DB 7; Length 44;  
Best Local Similarity 100.0%; Pred. No. 3.4e-15;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QOEKNEQELLELDKQASLWVWF 36  
Db 23 QOEKNEQELLELDKQASLWVWF 44

## RESULT 9

US-11-084-858-11  
; Sequence 11, Application US/11084858  
; Publication No. US2005021678A1  
; GENERAL INFORMATION:  
; APPLICANT: BRUST, Stefan  
; APPLICANT: KNAPP, Stefan  
; APPLICANT: GERKEN, Manfred  
; APPLICANT: GUERTLER, Lutz  
; TITLE OF INVENTION: Peptides derived from a retrovirus of  
; TITLE OF INVENTION: the HIV group, and their use  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/11/084,858  
; FILING DATE: 21-Mar-2005  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/10/000,321  
; FILING DATE: 04-Dec-2001  
; APPLICATION NUMBER: 09/131,551  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: SANDERCOCK, Colin G.  
; REGISTRATION NUMBER: 31,298  
; REFERENCE/DOCKET NUMBER: 58315/106/BEAK  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 145 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>

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;
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-11-084-858-11

Query Match      61.1%; Score 22; DB 7; Length 145;
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKWASLWNWF 36
Db 120 QQEKNEQELLELDKWASLWNWF 141

RESULT 10
US-10-506-796A-9
; Sequence 9, Application US/10506796A
; Publication No. US20060013831A1
; GENERAL INFORMATION:
; APPLICANT: MOR, Teafir
; APPLICANT: MATOBA, Nobuyuki
; APPLICANT: ARNTZEN, Charles
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ENHANCING IMMUNE RESPONSE
; FILE REFERENCE: 01231.0006U2
; CURRENT APPLICATION NUMBER: US/10/506,796A
; CURRENT FILING DATE: 2004-09-03
; PRIOR APPLICATION NUMBER: PCT/US03/07073
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: 60/362,247
; PRIOR FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence; note = synthetic construct
US-10-506-796A-9

Query Match      61.1%; Score 22; DB 6; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKWASLWNWF 36
Db 133 QQEKNEQELLELDKWASLWNWF 154

RESULT 11
US-10-841-956A-4
; Sequence 4, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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; OTHER INFORMATION: construct
US-10-841-956A-4

Query Match      61.1%; Score 22; DB 6; Length 267;
Best Local Similarity 100.0%; Pred. No. 1.9e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKWASLWNWF 36
Db 246 QQEKNEQELLELDKWASLWNWF 267

RESULT 12
US-10-841-956A-8
; Sequence 8, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-841-956A-8

Query Match      61.1%; Score 22; DB 6; Length 269;
Best Local Similarity 100.0%; Pred. No. 2e-14;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 QQEKNEQELLELDKWASLWNWF 36
Db 248 QQEKNEQELLELDKWASLWNWF 269

RESULT 13
US-10-841-956A-5
; Sequence 5, Application US/10841956A
; Publication No. US20050281829A1
; GENERAL INFORMATION:
; APPLICANT: TAN HEHIR, CRISTINA A.
; APPLICANT: MEZO, ADAM R.
; APPLICANT: PETERS, ROBERT T.
; APPLICANT: STATTEL, JAMES M.
; APPLICANT: PALOMBELLA, VITO J.
; APPLICANT: BITONTI, ALAN R.
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS
; FILE REFERENCE: 08945.0003-00000
; CURRENT APPLICATION NUMBER: US/10/841,956A
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: 60/468,835
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 270
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Peptide
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: construct  
US-10-841-956A-5

Query Match 61.1%; Score 22; DB 6; Length 270;  
Best Local Similarity 100.0%; Pred. No. 2e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 15 QOEKNEQELLELDKWSLWNWF 36  
Db 15 QOEKNEQELLELDKWSLWNWF 36

## RESULT 14

US-10-841-956A-7  
; Sequence 7, Application US/10841956A  
; Publication No. US20050281829A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN HEHIR, CRISTINA A.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: STATTEL, JAMES M.  
; APPLICANT: PALOMBELLA, VITO J.  
; APPLICANT: BITONTI, ALAN R.  
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS  
; FILE REFERENCE: 08945.0003-00000  
; CURRENT APPLICATION NUMBER: US/10/841,956A  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: 60/468,835  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 7  
; LENGTH: 281  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE: Peptide  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: construct  
US-10-841-956A-7

Query Match 61.1%; Score 22; DB 6; Length 281;  
Best Local Similarity 100.0%; Pred. No. 2e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 15 QOEKNEQELLELDKWSLWNWF 36  
Db 15 QOEKNEQELLELDKWSLWNWF 36

## RESULT 15

US-10-841-956A-6  
; Sequence 6, Application US/10841956A  
; Publication No. US20050281829A1  
; GENERAL INFORMATION:  
; APPLICANT: TAN HEHIR, CRISTINA A.  
; APPLICANT: MEZO, ADAM R.  
; APPLICANT: PETERS, ROBERT T.  
; APPLICANT: STATTEL, JAMES M.  
; APPLICANT: PALOMBELLA, VITO J.  
; APPLICANT: BITONTI, ALAN R.  
; TITLE OF INVENTION: FC CHIMERIC PROTEINS WITH ANTI-HIV DRUGS  
; FILE REFERENCE: 08945.0003-00000  
; CURRENT APPLICATION NUMBER: US/10/841,956A  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: 60/468,835  
; PRIOR FILING DATE: 2003-05-06  
; NUMBER OF SEQ ID NOS: 59  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 6  
; LENGTH: 282  
; TYPE: PRT  
; ORGANISM: Artificial Sequence

; FEATURE: Peptide  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: construct  
US-10-841-956A-6

Query Match 61.1%; Score 22; DB 6; Length 282;  
Best Local Similarity 100.0%; Pred. No. 2e-14;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 15 QOEKNEQELLELDKWSLWNWF 36  
Db 261 QOEKNEQELLELDKWSLWNWF 282

Search completed: March 6, 2006, 16:33:26  
Job time : 11.3333 secs

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